

## Sequence Listing

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Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
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Gerritsen, Mary E.  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, J. Christopher  
Gurney, Austin L.  
Kljavin, Ivar J.  
Napier, Mary A.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Watanabe, Colin K.  
Williams, P. Mickey  
Wood, William I.  
Zhang, Zemin

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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe  
 50 55 60  
 Tyr Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn  
 65 70 75  
 Leu Tyr Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala  
 80 85 90  
 Phe Asp Gly Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn  
 95 100 105

Trp	Ile	Cys	Ile	Val	Ile	Thr	Gly	Leu	Ala	Met	Asp	Met	Gln	Leu
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Leu	Met	Ile	Pro	Leu	Ile	Met	Ser	Val	Leu	Tyr	Val	Trp	Ala	Gln
				125					130					135
Leu	Asn	Arg	Asp	Met	Ile	Val	Ser	Phe	Trp	Phe	Gly	Thr	Arg	Phe
				140					145					150
Lys	Ala	Cys	Tyr	Leu	Pro	Trp	Val	Ile	Leu	Gly	Phe	Asn	Tyr	Ile
				155					160					165
Ile	Gly	Gly	Ser	Val	Ile	Asn	Glu	Leu	Ile	Gly	Asn	Leu	Val	Gly
				170					175					180
His	Leu	Tyr	Phe	Phe	Leu	Met	Phe	Arg	Tyr	Pro	Met	Asp	Leu	Gly
				185					190					195
Gly	Arg	Asn	Phe	Leu	Ser	Thr	Pro	Gln	Phe	Leu	Tyr	Arg	Trp	Leu
				200					205					210
Pro	Ser	Arg	Arg	Gly	Gly	Val	Ser	Gly	Phe	Gly	Val	Pro	Pro	Ala
				215					220					225
Ser	Met	Arg	Arg	Ala	Ala	Asp	Gln	Asn	Gly	Gly	Gly	Gly	Arg	His
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 <212> DNA  
 <213> Homo sapiens

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 gtccggcggt ctggcctagg gatcttcccc gttgcccctt tggggcgagg 200  
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 gggttcctgc gaggcccaga ctggtccatc cccatcttgg actttgtgga 300  
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 aagatcaatt tcaagaagca tgcacttctc ctcttgcaaa gaccataca 550  
 tcacaggcca ttttgcaacc tgtgttggca gcagaagatt ttactatctt 600  
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 gaataattca agagagaaat ggtgtattac ctgactgctt aaccgatggc 700

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 agtgaagctg caataatgaa taattcccaa ggggatgggtg aacattttgc 900  
 acaccacccc tcagaagtta aaatgcattt tgctaatacag tcaatagaac 950  
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 ggctgaaga ttctggctt agagcatgcg agcattgaag gaccaatagc 1050  
 aaacttatca gtacttgaa cagaagaact tcggcaacga gaacactatc 1100  
 tcaagcagaa gagagataag ttgatgtcca tgagaaagga tatgaggact 1150  
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 ggaaatgaca gagaaaccag aaatgacagc agaggagaag caaacattac 1250  
 taaagaggag attgcttgca gagaaactca aagaagaagt tattaataag 1300  
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<210> 8

<211> 367

<212> PRT

<213> Homo sapiens

<400> 8

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				20					25				30	
Asp	Phe	Val	Glu	Gln	Lys	Cys	Glu	Val	Asn	Cys	Lys	Gly	Gly	His
				35					40				45	
Val	Ile	Thr	Pro	Gly	Ser	Pro	Glu	Pro	Val	Ile	Leu	Val	Ala	Cys
				50					55				60	
Val	Pro	Leu	Val	Phe	Asp	Asp	Glu	Glu	Glu	Ser	Lys	Leu	Thr	Tyr
				65					70				75	
Thr	Glu	Ile	His	Gln	Glu	Tyr	Lys	Glu	Leu	Val	Glu	Lys	Leu	Leu
				80					85				90	
Glu	Gly	Tyr	Leu	Lys	Glu	Ile	Gly	Ile	Asn	Glu	Asp	Gln	Phe	Gln
				95					100				105	
Glu	Ala	Cys	Thr	Ser	Pro	Leu	Ala	Lys	Thr	His	Thr	Ser	Gln	Ala
				110					115				120	
Ile	Leu	Gln	Pro	Val	Leu	Ala	Ala	Glu	Asp	Phe	Thr	Ile	Phe	Lys
				125					130				135	
Ala	Met	Met	Val	Gln	Lys	Asn	Ile	Glu	Met	Gln	Leu	Gln	Ala	Ile
				140					145				150	

Arg	Ile	Ile	Gln	Glu	Arg	Asn	Gly	Val	Leu	Pro	Asp	Cys	Leu	Thr
				155					160					165
Asp	Gly	Ser	Asp	Val	Val	Ser	Asp	Leu	Glu	His	Glu	Glu	Met	Lys
				170					175					180
Ile	Leu	Arg	Glu	Val	Leu	Arg	Lys	Ser	Lys	Glu	Glu	Tyr	Asp	Gln
				185					190					195
Glu	Glu	Glu	Arg	Lys	Arg	Lys	Lys	Gln	Leu	Ser	Glu	Ala	Lys	Thr
				200					205					210
Glu	Glu	Pro	Thr	Val	His	Ser	Ser	Glu	Ala	Ala	Ile	Met	Asn	Asn
				215					220					225
Ser	Gln	Gly	Asp	Gly	Glu	His	Phe	Ala	His	Pro	Pro	Ser	Glu	Val
				230					235					240
Lys	Met	His	Phe	Ala	Asn	Gln	Ser	Ile	Glu	Pro	Leu	Gly	Arg	Lys
				245					250					255
Val	Glu	Arg	Ser	Glu	Thr	Ser	Ser	Leu	Pro	Gln	Lys	Gly	Leu	Lys
				260					265					270
Ile	Pro	Gly	Leu	Glu	His	Ala	Ser	Ile	Glu	Gly	Pro	Ile	Ala	Asn
				275					280					285
Leu	Ser	Val	Leu	Gly	Thr	Glu	Glu	Leu	Arg	Gln	Arg	Glu	His	Tyr
				290					295					300
Leu	Lys	Gln	Lys	Arg	Asp	Lys	Leu	Met	Ser	Met	Arg	Lys	Asp	Met
				305					310					315
Arg	Thr	Lys	Gln	Ile	Gln	Asn	Met	Glu	Gln	Lys	Gly	Lys	Pro	Thr
				320					325					330
Gly	Glu	Val	Glu	Glu	Met	Thr	Glu	Lys	Pro	Glu	Met	Thr	Ala	Glu
				335					340					345
Glu	Lys	Gln	Thr	Leu	Leu	Lys	Arg	Arg	Leu	Leu	Ala	Glu	Lys	Leu
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Lys	Glu	Glu	Val	Ile	Asn	Lys								
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<210> 9  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

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 aaggttacct caaagaaatt ggaattaatg aagatcaatt tcaagaagca 150  
 tgcacttctc ctcttgcaaa gacccataca tcacaggcca tttttgcaac 200  
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tggtgtatta cctgactgct taaccgatgg ctctgatgtg gtcagtgacc 350  
ttgaacacga agagatgaaa atcctgaggg aagttcttag aaaatcaaaa 400  
gaggaatatg accaggaa 418

<210> 10  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 10  
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<210> 11  
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<220>  
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<400> 11  
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<210> 12  
<211> 40  
<212> DNA  
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<223> Synthetic oligonucleotide probe

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<210> 13  
<211> 2886  
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<213> Homo sapiens

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cactagaagc tcttctgagg gaggtaatta aaaaacagtg gaatggaaaa 200  
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<210> 14

<211> 424

<212> PRT

<213> Homo sapiens

<400> 14

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				20					25					30
Ser	Ser	Arg	Ile	Leu	Leu	Val	Lys	Tyr	Ser	Ala	Asn	Glu	Glu	Asn
				35					40					45
Lys	Tyr	Asp	Tyr	Leu	Pro	Thr	Thr	Val	Asn	Val	Cys	Ser	Glu	Leu
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Val	Lys	Leu	Val	Phe	Cys	Val	Leu	Val	Ser	Phe	Cys	Val	Ile	Lys
				65					70					75
Lys	Asp	His	Gln	Ser	Arg	Asn	Leu	Lys	Tyr	Ala	Ser	Trp	Lys	Glu
				80					85					90
Phe	Ser	Asp	Phe	Met	Lys	Trp	Ser	Ile	Pro	Ala	Phe	Leu	Tyr	Phe
				95					100					105
Leu	Asp	Asn	Leu	Ile	Val	Phe	Tyr	Val	Leu	Ser	Tyr	Leu	Gln	Pro
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Ala	Met	Ala	Val	Ile	Phe	Ser	Asn	Phe	Ser	Ile	Ile	Thr	Thr	Ala	
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Leu	Leu	Phe	Arg	Ile	Val	Leu	Lys	Arg	Arg	Leu	Asn	Trp	Ile	Gln	
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Trp	Ala	Ser	Leu	Leu	Thr	Leu	Phe	Leu	Ser	Ile	Val	Ala	Leu	Thr	
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Ala	Gly	Thr	Lys	Thr	Leu	Gln	His	Asn	Leu	Ala	Gly	Arg	Gly	Phe	
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His	His	Asp	Ala	Phe	Phe	Ser	Pro	Ser	Asn	Ser	Cys	Leu	Leu	Phe	
				185					190					195	
Arg	Ser	Glu	Cys	Pro	Arg	Lys	Asp	Asn	Cys	Thr	Ala	Lys	Glu	Trp	
				200					205					210	
Thr	Phe	Pro	Glu	Ala	Lys	Trp	Asn	Thr	Thr	Ala	Arg	Val	Phe	Ser	
				215					220					225	
His	Ile	Arg	Leu	Gly	Met	Gly	His	Val	Leu	Ile	Ile	Val	Gln	Cys	
				230					235					240	
Phe	Ile	Ser	Ser	Met	Ala	Asn	Ile	Tyr	Asn	Glu	Lys	Ile	Leu	Lys	
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Glu	Gly	Asn	Gln	Leu	Thr	Glu	Ser	Ile	Phe	Ile	Gln	Asn	Ser	Lys	
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Leu	Tyr	Phe	Phe	Gly	Ile	Leu	Phe	Asn	Gly	Leu	Thr	Leu	Gly	Leu	
				275					280					285	
Gln	Arg	Ser	Asn	Arg	Asp	Gln	Ile	Lys	Asn	Cys	Gly	Phe	Phe	Tyr	
				290					295					300	
Gly	His	Ser	Ala	Phe	Ser	Val	Ala	Leu	Ile	Phe	Val	Thr	Ala	Phe	
				305					310					315	
Gln	Gly	Leu	Ser	Val	Ala	Phe	Ile	Leu	Lys	Phe	Leu	Asp	Asn	Met	
				320					325					330	
Phe	His	Val	Leu	Met	Ala	Gln	Val	Thr	Thr	Val	Ile	Ile	Thr	Thr	
				335					340					345	
Val	Ser	Val	Leu	Val	Phe	Asp	Phe	Arg	Pro	Ser	Leu	Glu	Phe	Phe	
				350					355					360	
Leu	Glu	Ala	Pro	Ser	Val	Leu	Leu	Ser	Ile	Phe	Ile	Tyr	Asn	Ala	
				365					370					375	
Ser	Lys	Pro	Gln	Val	Pro	Glu	Tyr	Ala	Pro	Arg	Gln	Glu	Arg	Ile	
				380					385					390	
Arg	Asp	Leu	Ser	Gly	Asn	Leu	Trp	Glu	Arg	Ser	Ser	Gly	Asp	Gly	
				395					400					405	
Glu	Glu	Leu	Glu	Arg	Leu	Thr	Lys	Pro	Lys	Ser	Asp	Glu	Ser	Asp	
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<212> DNA  
<213> Homo sapiens

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acagtgctgt agtcatcctg taatatgctc cttgtcaaca atgtatacat 300  
tcctgctagg tgccatattc attgctttaa gctcaagtgc catcttacta 350  
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cagccatggc tggtatcttc tcaaatttta gcattataac aacagctctt 650  
ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 700  
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cttta 755

<210> 16  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
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<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcagagaatt ccttcagga 20

<210> 18  
<211> 40  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

acagtgtgtg agtcatcctg taatatgctc cttgtcaaca 40

<210> 19

<211> 2142

<212> DNA

<213> Homo sapiens

<400> 19

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gcggcctgcg gggcagagga gcatcccgtc taccaggtcc caagcggcgt 150  
ggcccgcggg tcatggccaa aggagaaggc gccgagagcg gctccgcggc 200  
ggggctgcta cccaccagca tcctccaaag cactgaacgc ccggcccagg 250  
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gggtttcttc cttcagatct acctattgga tgtggctcag gtgggccctt 400  
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gacccccctg tgggcctctg catcagcaaa tccccctgga cctgcctggg 500  
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tacctgcttt tctattgcct ctttgaaaca atggtcacgt gtttccatgt 650  
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gattctgcca ccgcctatcg gatgactgtg gaagtgtctg gcacagtgt 750  
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gggggtcatt gtctgtatct atataatctg tgctgtcatc ctgatcctgg 950  
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gcctacttcc ggggcctacg gctggtcatg agccacggcc catacatcaa 1050  
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ggaactttgt cttgttttgc acctacacct tgggcttccg caatgaattc 1150  
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ctggcagtgg ttcttgacct ggtttgcaa gaagacagct gtatatgttg 1250

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 aacctcatca ttacatatgc ggtagctgtg gcagctggca tcagtgtggc 1350  
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 ggagaggcgg cggcagaata agaaggcctt gcaggcactg agggacgagg 1700  
 ccagcagctc tggctgtctc gaaacagact ccacagagct ggctagcatc 1750  
 ctctagggcc cgccacgttg cccgaagcca ccatgcagaa ggccacagaa 1800  
 gggatcagga cctgtctgcc ggcttgcctg gcagctggac tgcagggtgt 1850  
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 ggcctagccc ggaacactaa tgtagaaacc ttttttttac agagcctaata 2050  
 taataactta atgactgtgt acatagcaat gtgtgtgtat gtatatgtct 2100  
 gtgagctatt aatgttatta attttcataa aagctggaaa gc 2142

<210> 20  
 <211> 458  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
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 1 5 10 15  
 Trp Ala Glu Pro Gly Met Pro Ser Gln Thr Pro Trp Trp Ala Ser  
 20 25 30  
 Ala Ser Ala Asn Pro Pro Gly Pro Ala Trp Val Ala Leu Cys Pro  
 35 40 45  
 Gly Ser Ser Ser Pro Arg Pro Trp Pro Ser Leu Pro Thr Ser Ser  
 50 55 60  
 Ser Gly Ser Cys Pro Thr Ser His Thr Ala Arg Pro Ile Gly Thr  
 65 70 75  
 Cys Phe Ser Ile Ala Ser Leu Lys Gln Trp Ser Arg Val Ser Met  
 80 85 90  
 Phe Pro Thr Arg Leu Ser Pro Cys Ser Ser Ala Thr Glu Gln Thr  
 95 100 105

Glu Arg Asp Ser	Ala Thr Ala Tyr Arg	Met Thr Val Glu Val Leu	110	115	120
Gly Thr Val Leu	Gly Thr Ala Ile Gln	Gly Gln Ile Val Gly Gln	125	130	135
Ala Asp Thr Pro	Cys Phe Gln Asp Phe	Asn Ser Ser Thr Val Ala	140	145	150
Ser Gln Ser Ala	Asn His Thr His Gly	Thr Thr Ser His Arg Glu	155	160	165
Thr Gln Lys Ala	Tyr Leu Leu Ala Ala	Gly Val Ile Val Cys Ile	170	175	180
Tyr Ile Ile Cys	Ala Val Ile Leu Ile	Leu Gly Val Arg Glu Gln	185	190	195
Arg Glu Pro Tyr	Glu Ala Gln Gln Ser	Glu Pro Ile Ala Tyr Phe	200	205	210
Arg Gly Leu Arg	Leu Val Met Ser His	Gly Pro Tyr Ile Lys Leu	215	220	225
Ile Thr Gly Phe	Leu Phe Thr Ser Leu	Ala Phe Met Leu Val Glu	230	235	240
Gly Asn Phe Val	Leu Phe Cys Thr Tyr	Thr Leu Gly Phe Arg Asn	245	250	255
Glu Phe Gln Asn	Leu Leu Leu Ala Ile	Met Leu Ser Ala Thr Leu	260	265	270
Thr Ile Pro Ile	Trp Gln Trp Phe Leu	Thr Arg Phe Gly Lys Lys	275	280	285
Thr Ala Val Tyr	Val Gly Ile Ser Ser	Ala Val Pro Phe Leu Ile	290	295	300
Leu Val Ala Leu	Met Glu Ser Asn Leu	Ile Ile Thr Tyr Ala Val	305	310	315
Ala Val Ala Ala	Gly Ile Ser Val Ala	Ala Ala Phe Leu Leu Pro	320	325	330
Trp Ser Met Leu	Pro Asp Val Ile Asp	Asp Phe His Leu Lys Gln	335	340	345
Pro His Phe His	Gly Thr Glu Pro Ile	Phe Phe Ser Phe Tyr Val	350	355	360
Phe Phe Thr Lys	Phe Ala Ser Gly Val	Ser Leu Gly Ile Ser Thr	365	370	375
Leu Ser Leu Asp	Phe Ala Gly Tyr Gln	Thr Arg Gly Cys Ser Gln	380	385	390
Pro Glu Arg Val	Lys Phe Thr Leu Asn	Met Leu Val Thr Met Ala	395	400	405
Pro Ile Val Leu	Ile Leu Leu Gly Leu	Leu Leu Phe Lys Met Tyr	410	415	420

Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln  
425 430 435

Ala Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp  
440 445 450

Ser Thr Glu Leu Ala Ser Ile Leu  
455

<210> 21  
<211> 571  
<212> DNA  
<213> Homo sapiens

<400> 21  
gggaaacgca aaaggcatac ctgctggcag cgggggtcat tgtctgtatc 50  
tatataatct gtgctgtcat cctgatcctg ggcgctcgagg agcagagaga 100  
accctatgaa gccagcagct ctgagccaat cgcctacttc cggggcctac 150  
ggctgggtcat gagccacggc ccatacatca aacttattac tggcttcctc 200  
ttcacctcct tggctttcat gctgggtggag gggaaactttg tcttgttttg 250  
cacctacacc ttgggcttcc gcaatgaatt ccagaatcta ctcttgacca 300  
tcatgctctc ggccacttta accattccca tctggcagtg gttcttgacc 350  
cggtttgga agaagacagc tgtatatgtt gggatctcat cagcagtgcc 400  
atttctcatc ttgggtggcc tcatggagag taacctcatc attacatatg 450  
cggtagctgt ggcagctggc atcagtggtg cagctgcctt cttactaccc 500  
tgggtccatgc tgcctgatgt cattgacgac ttccatctga agcagcccca 550  
cttccatgga accgagccca t 571

<210> 22  
<211> 1173  
<212> DNA  
<213> Homo sapiens

<400> 22  
ggggcttcgg cgccagcggc cagcgctagt cggctctgga aggatttaca 50  
aaaggtgcag gtatgagcag gtctgaagac taacattttg tgaagttgta 100  
aaacagaaaa cctgttagaa atgtggtggt ttcagcaagg cctcagtttc 150  
cttccttcag cccttgtaat ttggacatct gctgctttca tattttcata 200  
cattactgca gtaacactcc accatataga cccggcttta cttatatca 250  
gtgacactgg tacagtagct ccagaaaaat gcttatttgg ggcaatgcta 300  
aatattgcgg cagttttatg cattgotacc atttatgttc gttataagca 350  
agttcatgct ctgagtcctg aagagaacgt tatcatcaaa ttaaacaagg 400  
ctggccttgt acttgaata ctgagttgtt taggactttc tattgtggca 450

aacttccaga aaacaaccct ttttgctgca catgtaagtg gagctgtgct 500  
taccttttggg atgggctcat tatatatgtt tgttcagacc atccttttcc 550  
accaaattgca gcccaaaatc catggcaaac aagtcttctg gatcagactg 600  
ttgttggtta tctgggtgtg agtaagtgca cttagcatgc tgacttgctc 650  
atcagttttg cacagtggca attttgggac tgatttagaa cagaaactcc 700  
attggaaccc cgaggacaaa ggttatgtgc ttcacatgat cactactgca 750  
gcagaatggg ctatgtcatt ttccttcttt ggttttttcc tgacttacat 800  
tcgtgatttt cagaaaattt ctttacgggt ggaagccaat ttacatggat 850  
taaccctcta tgacactgca ccttgcccta ttaacaatga acgaacacgg 900  
ctactttcca gagatatttg atgaaaggat aaaatatttc tgtaatgatt 950  
atgattctca gggattgggg aaaggttcac agaagttgct tattcttctc 1000  
tgaaattttc aaccacttaa tcaaggctga cagtaacaat gatgaatgct 1050  
gataatcagg aaacatgaaa gaagccattt gatagattat tctaaaggat 1100  
atcatcaaga agactattaa aaacacctat gcctatactt ttttatctca 1150  
gaaaataaag tcaaaagact atg 1173

<210> 23  
<211> 266  
<212> PRT  
<213> Homo sapiens

<400> 23  
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu  
1 5 10 15  
Val Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala  
20 25 30  
Val Thr Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp  
35 40 45  
Thr Gly Thr Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu  
50 55 60  
Asn Ile Ala Ala Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr  
65 70 75  
Lys Gln Val His Ala Leu Ser Pro Glu Glu Asn Val Ile Ile Lys  
80 85 90  
Leu Asn Lys Ala Gly Leu Val Leu Gly Ile Leu Ser Cys Leu Gly  
95 100 105  
Leu Ser Ile Val Ala Asn Phe Gln Lys Thr Thr Leu Phe Ala Ala  
110 115 120  
His Val Ser Gly Ala Val Leu Thr Phe Gly Met Gly Ser Leu Tyr  
125 130 135

Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	Gln	Met	Gln	Pro	Lys	Ile
				140					145					150
His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	Leu	Leu	Val	Ile	Trp
				155					160					165
Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	Ser	Ser	Val	Leu
				170					175					180
His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp
				185					190					195
Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Val	Leu	His	Met	Ile	Thr	Thr	Ala
				200					205					210
Ala	Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	Thr
				215					220					225
Tyr	Ile	Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn
				230					235					240
Leu	His	Gly	Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn
				245					250					255
Asn	Glu	Arg	Thr	Arg	Leu	Leu	Ser	Arg	Asp	Ile				
				260					265					

<210> 24  
 <211> 485  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 14, 484  
 <223> unknown base

<400> 24  
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 gagcggagat cctcaaacgg cctagtgcct cgcgcttcgg gagaaaatca 150  
 gcgggtctaataattcctct ggtttgttga agcagttacc aagaatcttc 200  
 aaccctttcc cacaaaagct aattgagtac acgttcctgt tgagtacacg 250  
 ttctgttga ttacaaaag gtgcaggtat gagcaggtct gaagactaac 300  
 attttgtgaa gttgtaaaac agaaaacctg ttagaaatgt ggtgggtttca 350  
 gcaaggcctc agtttccttc cttcagccct tgtaatttgg acatctgctg 400  
 ctttcatatt ttcatacatt actgcagtaa cactccacca tatagaccgg 450  
 gctttacctt atatcagtga cactggtaca gtanc 485

<210> 25  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
acctgttaga aatgtggtgg ttccagcaag gcctcagttt 40

<210> 26  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
ggagatagct gctatgggtt cttcaggcac aacttaacat gggaag 46

<210> 27  
<211> 1399  
<212> DNA  
<213> Homo sapiens

<400> 27  
cccacgcgtc cgcccgcgcg tgcgtcccgg agtgcaagtg agcttctcgg 50  
ctgccccgcg ggccgggggtg cggagccgac atgcgcccgc ttctcggcct 100  
ccttctggtc ttcgccgggt gcaccttcgc cttgtacttg ctgtcgacgc 150  
gactgccccg cgggcccgaga ctgggctcca ccgaggaggc tggaggcagg 200  
tcgctgtggt tcccctccga cctggcagag ctgcggggagc tctctgaggt 250  
ccttcgagag taccggaagg agcaccaggc ctacgtgttc ctgctcttct 300  
gcggcgccta cctctacaaa cagggttttg ccatccccgg ctccagcttc 350  
ctgaatgttt tagctggtgc cttgtttggg ccatggctgg ggcttctgct 400  
gtgctgtgtg ttgacctcgg tgggtgccac atgctgctac ctgctctcca 450  
gtatttttgg caaacagttg gtgggtgtcct actttcctga taaagtggcc 500  
ctgctgcaga gaaaggtgga ggagaacaga aacagcttgt ttttttctt 550  
attgtttttg agacttttcc ccatgacacc aaactgggtc ttgaacctct 600  
cggccccaat tctgaacatt cccatcgtgc agttcttctt ctcaagttctt 650  
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tatacacagt agaaaagaca catgatctgg attttctgtt tgccacatcc 900  
ctggactcag ttgcttattt gtgtaatgga tgtggctctc taaagcccct 950  
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tgcagtgtct tttcagaaag gacactctgc tcttgaaggt gtattacatc 1050  
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 agaaaatgct gtttgtggcc gggcgcggtg gctcacgcct gtaatcccag 1150  
 cactttggga ggccgaggcc ggtgattcac aaggtcagga gttcaagacc 1200  
 agcctggcca agatggtgaa atcctgtctc taataaaaat acaaaaatta 1250  
 gccaggcgtg gtggcaggca cctgtaatcc cagctactcg ggaggctgag 1300  
 gcaggagaat tgcttgaacc aaggtggcag aggttgcagt aagccaagat 1350  
 cacaccactg cactccagcc tgggtgatag agtgagacac tgtcttgac 1399

<210> 28

<211> 264

<212> PRT

<213> Homo sapiens

<400> 28

Met	Arg	Pro	Leu	Leu	Gly	Leu	Leu	Leu	Val	Phe	Ala	Gly	Cys	Thr	1	5	10	15
Phe	Ala	Leu	Tyr	Leu	Leu	Ser	Thr	Arg	Leu	Pro	Arg	Gly	Arg	Arg	20	25	30	
Leu	Gly	Ser	Thr	Glu	Glu	Ala	Gly	Gly	Arg	Ser	Leu	Trp	Phe	Pro	35	40	45	
Ser	Asp	Leu	Ala	Glu	Leu	Arg	Glu	Leu	Ser	Glu	Val	Leu	Arg	Glu	50	55	60	
Tyr	Arg	Lys	Glu	His	Gln	Ala	Tyr	Val	Phe	Leu	Leu	Phe	Cys	Gly	65	70	75	
Ala	Tyr	Leu	Tyr	Lys	Gln	Gly	Phe	Ala	Ile	Pro	Gly	Ser	Ser	Phe	80	85	90	
Leu	Asn	Val	Leu	Ala	Gly	Ala	Leu	Phe	Gly	Pro	Trp	Leu	Gly	Leu	95	100	105	
Leu	Leu	Cys	Cys	Val	Leu	Thr	Ser	Val	Gly	Ala	Thr	Cys	Cys	Tyr	110	115	120	
Leu	Leu	Ser	Ser	Ile	Phe	Gly	Lys	Gln	Leu	Val	Val	Ser	Tyr	Phe	125	130	135	
Pro	Asp	Lys	Val	Ala	Leu	Leu	Gln	Arg	Lys	Val	Glu	Glu	Asn	Arg	140	145	150	
Asn	Ser	Leu	Phe	Phe	Phe	Leu	Leu	Phe	Leu	Arg	Leu	Phe	Pro	Met	155	160	165	
Thr	Pro	Asn	Trp	Phe	Leu	Asn	Leu	Ser	Ala	Pro	Ile	Leu	Asn	Ile	170	175	180	
Pro	Ile	Val	Gln	Phe	Phe	Phe	Ser	Val	Leu	Ile	Gly	Leu	Ile	Pro	185	190	195	
Tyr	Asn	Phe	Ile	Cys	Val	Gln	Thr	Gly	Ser	Ile	Leu	Ser	Thr	Leu	200	205	210	

Thr	Ser	Leu	Asp	Ala	Leu	Phe	Ser	Trp	Asp	Thr	Val	Phe	Lys	Leu
				215					220					225
Leu	Ala	Ile	Ala	Met	Val	Ala	Leu	Ile	Pro	Gly	Thr	Leu	Ile	Lys
				230					235					240
Lys	Phe	Ser	Gln	Lys	His	Leu	Gln	Leu	Asn	Glu	Thr	Ser	Thr	Ala
				245					250					255
Asn	His	Ile	His	Ser	Arg	Lys	Asp	Thr						
				260										

<210> 29  
 <211> 1292  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 ccgaggcggg aggagcccgga gggggcgcgga gccccgcgatg aatcattgta 50  
 gtcaatcatt ttccagttct cagccgctca gttgtgatca agggacacgt 100  
 ggtttccgaa ctgccagctc agaataggaa aataacttgg gattttatat 150  
 tggaagacat ggatcttgct gccaacgaga tcagcattta tgacaaactt 200  
 tcagagactg ttgatttggt gagacagacc ggccatcagt gtggcatgtc 250  
 agagaaggca attgaaaaat ttatcagaca gctgctggaa aagaatgaac 300  
 ctgagagacc ccccccgag tatcctctcc ttatagttgt gtataagggt 350  
 ctgcgaacct tgggattaat cttgctcact gcctactttg tgattcaacc 400  
 tttcagccca ttagcacctg agccagtgtt ttctggagct cacacctggc 450  
 gctcactcat ccatcacatt aggctgatgt ccttgcccat tgccaagaag 500  
 tacatgtcag aaaataaggg agttcctctg catgggggtg atgaagacag 550  
 accctttcca gactttgacc cctggtggac aaacgactgt gaggagaatg 600  
 agtcagagcc cattcctgcc aactgcactg gctgtgcca gaaacacctg 650  
 aaggtgatgc tcctggaaga cggcccaagg aaatttgaga ggctccatcc 700  
 actggtgatc aagacgggaa agcccctgtt ggaggaagag attcagcatt 750  
 ttttgtgcca gtaccctgag gcgacagaag gcttctctga aggggttttc 800  
 gccaaagtggg ggcgctgctt tcctgagcgg tggttcccat ttccttatcc 850  
 atggaggaga cctctgaaca gatcacaat gttacgtgag ctttttctctg 900  
 ttttcaactca cctgccattt ccaaagatg cctctttaa caagtgtcc 950  
 tttcttcacc cagaacctgt tgtggggagt aagatgcata agatgcctga 1000  
 cctattttatc attggcagcg gtgaggccat gttgcagctc atccctccct 1050  
 tccagtgccg aagacattgt cagtctgtgg ccatgccaat agagccaggg 1100  
 gatatcggct atgtcgacac caccactgg aaggctctacg ttatagccag 1150

aggggtccag cctttggtca tctgcatgg aaccgcttcc tcagaactgt 1200  
 aggaaataga actgtgcaca ggaacagctt ccagagccga aaaccagggt 1250  
 gaaaggggaa aaataaaaaac aaaaacgatg aaactgcaaa aa 1292

<210> 30  
 <211> 347  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Met Asp Leu Ala Ala Asn Glu Ile Ser Ile Tyr Asp Lys Leu Ser  
 1 5 10 15  
 Glu Thr Val Asp Leu Val Arg Gln Thr Gly His Gln Cys Gly Met  
 20 25 30  
 Ser Glu Lys Ala Ile Glu Lys Phe Ile Arg Gln Leu Leu Glu Lys  
 35 40 45  
 Asn Glu Pro Gln Arg Pro Pro Pro Gln Tyr Pro Leu Leu Ile Val  
 50 55 60  
 Val Tyr Lys Val Leu Ala Thr Leu Gly Leu Ile Leu Leu Thr Ala  
 65 70 75  
 Tyr Phe Val Ile Gln Pro Phe Ser Pro Leu Ala Pro Glu Pro Val  
 80 85 90  
 Leu Ser Gly Ala His Thr Trp Arg Ser Leu Ile His His Ile Arg  
 95 100 105  
 Leu Met Ser Leu Pro Ile Ala Lys Lys Tyr Met Ser Glu Asn Lys  
 110 115 120  
 Gly Val Pro Leu His Gly Gly Asp Glu Asp Arg Pro Phe Pro Asp  
 125 130 135  
 Phe Asp Pro Trp Trp Thr Asn Asp Cys Glu Gln Asn Glu Ser Glu  
 140 145 150  
 Pro Ile Pro Ala Asn Cys Thr Gly Cys Ala Gln Lys His Leu Lys  
 155 160 165  
 Val Met Leu Leu Glu Asp Ala Pro Arg Lys Phe Glu Arg Leu His  
 170 175 180  
 Pro Leu Val Ile Lys Thr Gly Lys Pro Leu Leu Glu Glu Glu Ile  
 185 190 195  
 Gln His Phe Leu Cys Gln Tyr Pro Glu Ala Thr Glu Gly Phe Ser  
 200 205 210  
 Glu Gly Phe Phe Ala Lys Trp Trp Arg Cys Phe Pro Glu Arg Trp  
 215 220 225  
 Phe Pro Phe Pro Tyr Pro Trp Arg Arg Pro Leu Asn Arg Ser Gln  
 230 235 240  
 Met Leu Arg Glu Leu Phe Pro Val Phe Thr His Leu Pro Phe Pro  
 245 250 255

Lys	Asp	Ala	Ser	Leu	Asn	Lys	Cys	Ser	Phe	Leu	His	Pro	Glu	Pro
				260					265					270
Val	Val	Gly	Ser	Lys	Met	His	Lys	Met	Pro	Asp	Leu	Phe	Ile	Ile
				275					280					285
Gly	Ser	Gly	Glu	Ala	Met	Leu	Gln	Leu	Ile	Pro	Pro	Phe	Gln	Cys
				290					295					300
Arg	Arg	His	Cys	Gln	Ser	Val	Ala	Met	Pro	Ile	Glu	Pro	Gly	Asp
				305					310					315
Ile	Gly	Tyr	Val	Asp	Thr	Thr	His	Trp	Lys	Val	Tyr	Val	Ile	Ala
				320					325					330
Arg	Gly	Val	Gln	Pro	Leu	Val	Ile	Cys	Asp	Gly	Thr	Ala	Phe	Ser
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Glu Leu

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 <211> 478  
 <212> DNA  
 <213> Homo sapiens

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 agctcagaat aggaaaataa cttgggattt tatattggaa gacatggatc 200  
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 cgcagtatcc tctccttata gttgtgtata aggttctcgc aaccttgga 400  
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 acctgagcca gtgctttgtg gagctcac 478

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 <211> 3531  
 <212> DNA  
 <213> Homo sapiens

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 gcagagcgct gctcctggct ggtgccactg gtgcgcacgc tgetagaccg 150  
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cccgaatggc gccacttcat cgacaaacag gtacagccaa ccatgtccca 300  
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 ggaatgacctg ctatgacatg cttatgagca gtgggcagcg gcgccagtgg 400  
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gttaccct cagggattgg cgggcggaag tcccggccct cgccggctga 3500  
 ggggccgccc tgaggccag cactggcgtc t 3531

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 <212> PRT  
 <213> Homo sapiens

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 Gly Gln Arg Arg Gln Trp Glu Arg Ala Gln Ser Arg Arg Ala Phe  
 35 40 45  
 Gln Glu Leu Val Leu Glu Pro Ala Gln Arg Arg Ala Arg Leu Glu  
 50 55 60  
 Gly Leu Arg Tyr Thr Ala Val Leu Lys Gln Gln Ala Thr Gln His  
 65 70 75  
 Ser Met Ala Leu Leu His Trp Gly Ala Leu Trp Arg Gln Leu Ala  
 80 85 90  
 Ser Pro Cys Gly Ala Trp Ala Leu Arg Asp Thr Pro Ile Pro Arg  
 95 100 105  
 Trp Lys Leu Ser Ser Ala Glu Thr Tyr Ser Arg Met Arg Leu Lys  
 110 115 120  
 Leu Val Pro Asn His His Phe Asp Pro His Leu Glu Ala Ser Ala  
 125 130 135  
 Leu Arg Asp Asn Leu Gly Glu Val Pro Leu Thr Pro Thr Glu Glu  
 140 145 150  
 Ala Ser Leu Pro Leu Ala Val Thr Lys Glu Ala Lys Val Ser Thr  
 155 160 165  
 Pro Pro Glu Leu Leu Gln Glu Asp Gln Leu Gly Glu Asp Glu Leu  
 170 175 180  
 Ala Glu Leu Glu Thr Pro Met Glu Ala Ala Glu Leu Asp Glu Gln  
 185 190 195  
 Arg Glu Lys Leu Val Leu Ser Ala Glu Cys Gln Leu Val Thr Val  
 200 205 210  
 Val Ala Val Val Pro Gly Leu Leu Glu Val Thr Thr Gln Asn Val  
 215 220 225  
 Tyr Phe Tyr Asp Gly Ser Thr Glu Arg Val Glu Thr Glu Glu Gly  
 230 235 240  
 Ile Gly Tyr Asp Phe Arg Arg Pro Leu Ala Gln Leu Arg Glu Val  
 245 250 255  
 His Leu Arg Arg Phe Asn Leu Arg Arg Ser Ala Leu Glu Leu Phe  
 260 265 270

Phe	Ile	Asp	Gln	Ala	Asn	Tyr	Phe	Leu	Asn	Phe	Pro	Cys	Lys	Val	
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Gly	Thr	Thr	Pro	Val	Ser	Ser	Pro	Ser	Gln	Thr	Pro	Arg	Pro	Gln	
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Pro	Gly	Pro	Ile	Pro	Pro	His	Thr	Gln	Val	Arg	Asn	Gln	Val	Tyr	
				305					310					315	
Ser	Trp	Leu	Leu	Arg	Leu	Arg	Pro	Pro	Ser	Gln	Gly	Tyr	Leu	Ser	
				320					325					330	
Ser	Arg	Ser	Pro	Gln	Glu	Met	Leu	Arg	Ala	Ser	Gly	Leu	Thr	Gln	
				335					340					345	
Lys	Trp	Val	Gln	Arg	Glu	Ile	Ser	Asn	Phe	Glu	Tyr	Leu	Met	Gln	
				350					355					360	
Leu	Asn	Thr	Ile	Ala	Gly	Arg	Thr	Tyr	Asn	Asp	Leu	Ser	Gln	Tyr	
				365					370					375	
Pro	Val	Phe	Pro	Trp	Val	Leu	Gln	Asp	Tyr	Val	Ser	Pro	Thr	Leu	
				380					385					390	
Asp	Leu	Ser	Asn	Pro	Ala	Val	Phe	Arg	Asp	Leu	Ser	Lys	Pro	Ile	
				395					400					405	
Gly	Val	Val	Asn	Pro	Lys	His	Ala	Gln	Leu	Val	Arg	Glu	Lys	Tyr	
				410					415					420	
Glu	Ser	Phe	Glu	Asp	Pro	Ala	Gly	Thr	Ile	Asp	Lys	Phe	His	Tyr	
				425					430					435	
Gly	Thr	His	Tyr	Ser	Asn	Ala	Ala	Gly	Val	Met	His	Tyr	Leu	Ile	
				440					445					450	
Arg	Val	Glu	Pro	Phe	Thr	Ser	Leu	His	Val	Gln	Leu	Gln	Ser	Gly	
				455					460					465	
Arg	Phe	Asp	Cys	Ser	Asp	Arg	Gln	Phe	His	Ser	Val	Ala	Ala	Ala	
				470					475					480	
Trp	Gln	Ala	Arg	Leu	Glu	Ser	Pro	Ala	Asp	Val	Lys	Glu	Leu	Ile	
				485					490					495	
Pro	Glu	Phe	Phe	Tyr	Phe	Pro	Asp	Phe	Leu	Glu	Asn	Gln	Asn	Gly	
				500					505					510	
Phe	Asp	Leu	Gly	Cys	Leu	Gln	Leu	Thr	Asn	Glu	Lys	Val	Gly	Asp	
				515					520					525	
Val	Val	Leu	Pro	Pro	Trp	Ala	Ser	Ser	Pro	Glu	Asp	Phe	Ile	Gln	
				530					535					540	
Gln	His	Arg	Gln	Ala	Leu	Glu	Ser	Glu	Tyr	Val	Ser	Ala	His	Leu	
				545					550					555	
His	Glu	Trp	Ile	Asp	Leu	Ile	Phe	Gly	Tyr	Lys	Gln	Arg	Gly	Pro	
				560					565					570	
Ala	Ala	Glu	Glu	Ala	Leu	Asn	Val	Phe	Tyr	Tyr	Cys	Thr	Tyr	Glu	
				575					580					585	

Gly	Ala	Val	Asp	Leu	Asp	His	Val	Thr	Asp	Glu	Arg	Glu	Arg	Lys	
				590					595					600	
Ala	Leu	Glu	Gly	Ile	Ile	Ser	Asn	Phe	Gly	Gln	Thr	Pro	Cys	Gln	
				605					610					615	
Leu	Leu	Lys	Glu	Pro	His	Pro	Thr	Arg	Leu	Ser	Ala	Glu	Glu	Ala	
				620					625					630	
Ala	His	Arg	Leu	Ala	Arg	Leu	Asp	Thr	Asn	Ser	Pro	Ser	Ile	Phe	
				635					640					645	
Gln	His	Leu	Asp	Glu	Leu	Lys	Ala	Phe	Phe	Ala	Glu	Val	Thr	Val	
				650					655					660	
Ser	Ala	Ser	Gly	Leu	Leu	Gly	Thr	His	Ser	Trp	Leu	Pro	Tyr	Asp	
				665					670					675	
Arg	Asn	Ile	Ser	Asn	Tyr	Phe	Ser	Phe	Ser	Lys	Asp	Pro	Thr	Met	
				680					685					690	
Gly	Ser	His	Lys	Thr	Gln	Arg	Leu	Leu	Ser	Gly	Pro	Trp	Val	Pro	
				695					700					705	
Gly	Ser	Gly	Val	Ser	Gly	Gln	Ala	Leu	Ala	Val	Ala	Pro	Asp	Gly	
				710					715					720	
Lys	Leu	Leu	Phe	Ser	Gly	Gly	His	Trp	Asp	Gly	Ser	Leu	Arg	Val	
				725					730					735	
Thr	Ala	Leu	Pro	Arg	Gly	Lys	Leu	Leu	Ser	Gln	Leu	Ser	Cys	His	
				740					745					750	
Leu	Asp	Val	Val	Thr	Cys	Leu	Ala	Leu	Asp	Thr	Cys	Gly	Ile	Tyr	
				755					760					765	
Leu	Ile	Ser	Gly	Ser	Arg	Asp	Thr	Thr	Cys	Met	Val	Trp	Arg	Leu	
				770					775					780	
Leu	His	Gln	Gly	Gly	Leu	Ser	Val	Gly	Leu	Ala	Pro	Lys	Pro	Val	
				785					790					795	
Gln	Val	Leu	Tyr	Gly	His	Gly	Ala	Ala	Val	Ser	Cys	Val	Ala	Ile	
				800					805					810	
Ser	Thr	Glu	Leu	Asp	Met	Ala	Val	Ser	Gly	Ser	Glu	Asp	Gly	Thr	
				815					820					825	
Val	Ile	Ile	His	Thr	Val	Arg	Arg	Gly	Gln	Phe	Val	Ala	Ala	Leu	
				830					835					840	
Arg	Pro	Leu	Gly	Ala	Thr	Phe	Pro	Gly	Pro	Ile	Phe	His	Leu	Ala	
				845					850					855	
Leu	Gly	Ser	Glu	Gly	Gln	Ile	Val	Val	Gln	Ser	Ser	Ala	Trp	Glu	
				860					865					870	
Arg	Pro	Gly	Ala	Gln	Val	Thr	Tyr	Ser	Leu	His	Leu	Tyr	Ser	Val	
				875					880					885	
Asn	Gly	Lys	Leu	Arg	Ala	Ser	Leu	Pro	Leu	Ala	Glu	Gln	Pro	Thr	
				890					895					900	

Ala	Leu	Thr	Val	Thr	Glu	Asp	Phe	Val	Leu	Leu	Gly	Thr	Ala	Gln	
				905					910					915	
Cys	Ala	Leu	His	Ile	Leu	Gln	Leu	Asn	Thr	Leu	Leu	Pro	Ala	Ala	
				920					925					930	
Pro	Pro	Leu	Pro	Met	Lys	Val	Ala	Ile	Arg	Ser	Val	Ala	Val	Thr	
				935					940					945	
Lys	Glu	Arg	Ser	His	Val	Leu	Val	Gly	Leu	Glu	Asp	Gly	Lys	Leu	
				950					955					960	
Ile	Val	Val	Val	Ala	Gly	Gln	Pro	Ser	Glu	Val	Arg	Ser	Ser	Gln	
				965					970					975	
Phe	Ala	Arg	Lys	Leu	Trp	Arg	Ser	Ser	Arg	Arg	Ile	Ser	Gln	Val	
				980					985					990	
Ser	Ser	Gly	Glu	Thr	Glu	Tyr	Asn	Pro	Thr	Glu	Ala	Arg			
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 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 35  
 <211> 1395  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
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 ttcaatctgc aaatctatgg ggtcctgggg ctcttctgga cccttaactg 200  
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<210> 36

<211> 321

<212> PRT

<213> Homo sapiens

<400> 36

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				20					25					30
Pro	Gly	Leu	Met	Cys	Val	Phe	Gln	Gly	Tyr	Ser	Ser	Lys	Gly	Leu
				35					40					45
Ile	Gln	Arg	Ser	Val	Phe	Asn	Leu	Gln	Ile	Tyr	Gly	Val	Leu	Gly
				50					55					60
Leu	Phe	Trp	Thr	Leu	Asn	Trp	Val	Leu	Ala	Leu	Gly	Gln	Cys	Val
				65					70					75
Leu	Ala	Gly	Ala	Phe	Ala	Ser	Phe	Tyr	Trp	Ala	Phe	His	Lys	Pro
				80					85					90
Gln	Asp	Ile	Pro	Thr	Phe	Pro	Leu	Ile	Ser	Ala	Phe	Ile	Arg	Thr
				95					100					105
Leu	Arg	Tyr	His	Thr	Gly	Ser	Leu	Ala	Phe	Gly	Ala	Leu	Ile	Leu
				110					115					120
Thr	Leu	Val	Gln	Ile	Ala	Arg	Val	Ile	Leu	Glu	Tyr	Ile	Asp	His
				125					130					135

Lys	Leu	Arg	Gly	Val	Gln	Asn	Pro	Val	Ala	Arg	Cys	Ile	Met	Cys	
				140					145					150	
Cys	Phe	Lys	Cys	Cys	Leu	Trp	Cys	Leu	Glu	Lys	Phe	Ile	Lys	Phe	
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Leu	Asn	Arg	Asn	Ala	Tyr	Ile	Met	Ile	Ala	Ile	Tyr	Gly	Lys	Asn	
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Phe	Cys	Val	Ser	Ala	Lys	Asn	Ala	Phe	Met	Leu	Leu	Met	Arg	Asn	
				185					190					195	
Ile	Val	Arg	Val	Val	Val	Leu	Asp	Lys	Val	Thr	Asp	Leu	Leu	Leu	
				200					205					210	
Phe	Phe	Gly	Lys	Leu	Leu	Val	Val	Gly	Gly	Val	Gly	Val	Leu	Ser	
				215					220					225	
Phe	Phe	Phe	Phe	Ser	Gly	Arg	Ile	Pro	Gly	Leu	Gly	Lys	Asp	Phe	
				230					235					240	
Lys	Ser	Pro	His	Leu	Asn	Tyr	Tyr	Trp	Leu	Pro	Ile	Met	Thr	Ser	
				245					250					255	
Ile	Leu	Gly	Ala	Tyr	Val	Ile	Ala	Ser	Gly	Phe	Phe	Ser	Val	Phe	
				260					265					270	
Gly	Met	Cys	Val	Asp	Thr	Leu	Phe	Leu	Cys	Phe	Leu	Glu	Asp	Leu	
				275					280					285	
Glu	Arg	Asn	Asn	Gly	Ser	Leu	Asp	Arg	Pro	Tyr	Tyr	Met	Ser	Lys	
				290					295					300	
Ser	Leu	Leu	Lys	Ile	Leu	Gly	Lys	Lys	Asn	Glu	Ala	Pro	Pro	Asp	
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Asn	Lys	Lys	Arg	Lys	Lys										
				320											

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<220>  
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<400> 37  
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<210> 38  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 38  
 gtctttaccc agccccggga tgcg 24

<210> 39  
 <211> 50

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 39  
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<210> 40  
<211> 1365  
<212> DNA  
<213> Homo sapiens

<400> 40  
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agggtggtcca gagccagagg gtccttctct tcgtggcctc ggacgtggat 150  
gctctgtgtg cgtgcaagat ccttcaggcc ttgttcaggt gtgaccacgt 200  
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 <211> 566  
 <212> PRT  
 <213> Homo sapiens

<400> 41  
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 Gln Tyr Thr Leu Val Pro Val Ser Gly Trp Gln Glu Leu Glu Thr  
 50 55 60  
 Ala Phe Leu Glu His Lys Glu Gln Phe His Tyr Phe Ile Leu Ile  
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 80 85 90  
 Glu Asp Thr Ile Phe Phe Val Cys Asp Ser His Arg Pro Val Asn  
 95 100 105  
 Val Val Asn Val Tyr Asn Asp Thr Gln Ile Lys Leu Leu Ile Lys  
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 Gln Asp Asp Asp Leu Glu Val Pro Ala Tyr Glu Asp Ile Phe Arg  
 125 130 135  
 Asp Glu Glu Glu Asp Glu Glu His Ser Gly Asn Asp Ser Asp Gly  
 140 145 150  
 Ser Glu Pro Ser Glu Lys Arg Thr Arg Leu Glu Glu Glu Ile Val  
 155 160 165  
 Glu Gln Thr Met Arg Arg Arg Gln Arg Arg Glu Trp Glu Ala Arg  
 170 175 180  
 Arg Arg Asp Ile Leu Phe Asp Tyr Glu Gln Tyr Glu Tyr His Gly  
 185 190 195  
 Thr Ser Ser Ala Met Val Met Phe Glu Leu Ala Trp Met Leu Ser  
 200 205 210  
 Lys Asp Leu Asn Asp Met Leu Trp Trp Ala Ile Val Gly Leu Thr  
 215 220 225  
 Asp Gln Trp Val Gln Asp Lys Ile Thr Gln Met Lys Tyr Val Thr  
 230 235 240  
 Asp Val Gly Val Leu Gln Arg His Val Ser Arg His Asn His Arg

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Ser Phe Glu Tyr	Asp Leu Arg Leu Val	Leu Tyr Gln His Trp	Ser
	275	280	285
Leu His Asp Ser	Leu Cys Asn Thr Ser	Tyr Thr Ala Ala Arg	Phe
	290	295	300
Lys Leu Trp Ser	Val His Gly Gln Lys	Arg Leu Gln Glu Phe	Leu
	305	310	315
Ala Asp Met Gly	Leu Pro Leu Lys Gln	Val Lys Gln Lys Phe	Gln
	320	325	330
Ala Met Asp Ile	Ser Leu Lys Glu Asn	Leu Arg Glu Met Ile	Glu
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Glu Ser Ala Asn	Lys Phe Gly Met Lys	Asp Met Arg Val Gln	Thr
	350	355	360
Phe Ser Ile His	Phe Gly Phe Lys His	Lys Phe Leu Ala Ser	Asp
	365	370	375
Val Val Phe Ala	Thr Met Ser Leu Met	Glu Ser Pro Glu Lys	Asp
	380	385	390
Gly Ser Gly Thr	Asp His Phe Ile Gln	Ala Leu Asp Ser Leu	Ser
	395	400	405
Arg Ser Asn Leu	Asp Lys Leu Tyr His	Gly Leu Glu Leu Ala	Lys
	410	415	420
Lys Gln Leu Arg	Ala Thr Gln Gln Thr	Ile Ala Ser Cys Leu	Cys
	425	430	435
Thr Asn Leu Val	Ile Ser Gln Gly Pro	Phe Leu Tyr Cys Ser	Leu
	440	445	450
Met Glu Gly Thr	Pro Asp Val Met Leu	Phe Ser Arg Pro Ala	Ser
	455	460	465
Leu Ser Leu Leu	Ser Lys His Leu Leu	Lys Ser Phe Val Cys	Ser
	470	475	480
Thr Lys Asn Arg	Arg Cys Lys Leu Leu	Pro Leu Val Met Ala	Ala
	485	490	495
Pro Leu Ser Met	Glu His Gly Thr Val	Thr Val Val Gly Ile	Pro
	500	505	510
Pro Glu Thr Asp	Ser Ser Asp Arg Lys	Asn Phe Phe Gly Arg	Ala
	515	520	525
Phe Glu Lys Ala	Ala Glu Ser Thr Ser	Ser Arg Met Leu His	Asn
	530	535	540
His Phe Asp Leu	Ser Val Ile Glu Leu	Lys Ala Glu Asp Arg	Ser
	545	550	555
Lys Phe Leu Asp	Ala Leu Ile Ser Leu	Leu Ser	

<210> 42  
 <211> 380  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 44, 118, 172, 183  
 <223> unknown base

<400> 42  
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 ctcttcgtgg cctcggangt ggatgctctg tgtgcgtgca agatccttca 150  
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 ggtggcaaga acttgaaact gcatttcttg agcataaaga acagtttcat 250  
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<210> 43  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 43  
 ttccgcaaag agttctacga ggtgg 25

<210> 44  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 44  
 attgacaaca ttgactggcc tatggg 26

<210> 45  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 45  
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<210> 46

<211> 3089  
<212> DNA  
<213> Homo sapiens

<400> 46

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<210> 47

<211> 259

<212> PRT

<213> Homo sapiens

<220>

<221> Signal Peptide

<222> 1-20

<223> Signal Peptide

<220>

<221> N-glycosylation Site

<222> 72-75

<223> N-glycosylation Site

<220>

<221> Clq Domain Proteins

<222> 144-178, 78-111, 84-117

<223> Clq Domain Proteins

<400> 47

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20 25 30

Arg Ala Val Ala Ser Gly Cys Gln Arg Cys Cys Asp Ser Glu Asp  
35 40 45

Pro Leu Asp Pro Ala His Val Ser Ser Ala Ser Ser Ser Gly Arg  
50 55 60

Pro His Ala Leu Pro Glu Ile Arg Pro Tyr Ile Asn Ile Thr Ile  
65 70 75

Leu Lys Gly Asp Lys Gly Asp Pro Gly Pro Met Gly Leu Pro Gly  
80 85 90

Tyr Met Gly Arg Glu Gly Pro Gln Gly Glu Pro Gly Pro Gln Gly  
95 100 105

Ser Lys Gly Asp Lys Gly Glu Met Gly Ser Pro Gly Ala Pro Cys  
110 115 120

Gln Lys Arg Phe Phe Ala Phe Ser Val Gly Arg Lys Thr Ala Leu  
125 130 135

His Ser Gly Glu Asp Phe Gln Thr Leu Leu Phe Glu Arg Val Phe  
140 145 150

Val Asn Leu Asp Gly Cys Phe Asp Met Ala Thr Gly Gln Phe Ala  
155 160 165

Ala Pro Leu Arg Gly Ile Tyr Phe Phe Ser Leu Asn Val His Ser  
170 175 180

Trp Asn Tyr Lys Glu Thr Tyr Val His Ile Met His Asn Gln Lys  
185 190 195

Glu Ala Val Ile Leu Tyr Ala Gln Pro Ser Glu Arg Ser Ile Met

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Gln Ser Gln Ser	Val Met Leu Asp Leu	Ala Tyr Gly Asp Arg	Val
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Trp Val Arg Leu	Phe Lys Arg Gln Arg	Glu Asn Ala Ile Tyr	Ser
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Asn Asp Phe Asp	Thr Tyr Ile Thr Phe	Ser Gly His Leu Ile	Lys
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<210> 48  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 48  
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<210> 49  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 49  
 ggtccccgta ggccaggtcc agc 23

<210> 50  
 <211> 50  
 <212> DNA  
 <213> Artificial sequence

<220>  
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<400> 50  
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<210> 51  
 <211> 2768  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
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<210> 52  
 <211> 673  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
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 Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr  
 35 40 45  
 Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe  
 50 55 60  
 Glu Asn Gly Ile Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu  
 65 70 75  
 Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser  
 80 85 90  
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Asp Leu Thr Ala	Asn Arg Leu His Glu	Ile Thr Asn Glu Thr	Phe
	110	115	120
Arg Gly Leu Arg	Arg Leu Glu Arg Leu	Tyr Leu Gly Lys Asn	Arg
	125	130	135
Ile Arg His Ile	Gln Pro Gly Ala Phe	Asp Thr Leu Asp Arg	Leu
	140	145	150
Leu Glu Leu Lys	Leu Gln Asp Asn Glu	Leu Arg Ala Leu Pro	Pro
	155	160	165
Leu Arg Leu Pro	Arg Leu Leu Leu Leu	Asp Leu Ser His Asn	Ser
	170	175	180
Leu Leu Ala Leu	Glu Pro Gly Ile Leu	Asp Thr Ala Asn Val	Glu
	185	190	195
Ala Leu Arg Leu	Ala Gly Leu Gly Leu	Gln Gln Leu Asp Glu	Gly
	200	205	210
Leu Phe Ser Arg	Leu Arg Asn Leu His	Asp Leu Asp Val Ser	Asp
	215	220	225
Asn Gln Leu Glu	Arg Val Pro Pro Val	Ile Arg Gly Leu Arg	Gly
	230	235	240
Leu Thr Arg Leu	Arg Leu Ala Gly Asn	Thr Arg Ile Ala Gln	Leu
	245	250	255
Arg Pro Glu Asp	Leu Ala Gly Leu Ala	Ala Leu Gln Glu Leu	Asp
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Val Ser Asn Leu	Ser Leu Gln Ala Leu	Pro Gly Asp Leu Ser	Gly
	275	280	285
Leu Phe Pro Arg	Leu Arg Leu Leu Ala	Ala Ala Arg Asn Pro	Phe
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Ser His Val Thr	Leu Ala Ser Pro Glu	Glu Thr Arg Cys His	Phe
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Pro Pro Lys Asn	Ala Gly Arg Leu Leu	Leu Glu Leu Asp Tyr	Ala
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Asp Phe Gly Cys	Pro Ala Thr Thr Thr	Thr Ala Thr Val Pro	Thr
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Thr Arg Pro Val	Val Arg Glu Pro Thr	Ala Leu Ser Ser Ser	Leu
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Ala Pro Thr Trp	Leu Ser Pro Thr Ala	Pro Ala Thr Glu Ala	Pro
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	395	400	405
Pro Gln Asp Cys	Pro Pro Ser Thr Cys	Leu Asn Gly Gly Thr	Cys

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His Leu Gly Thr	Arg His His Leu Ala	Cys Leu Cys Pro Glu	Gly
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Phe Thr Gly Leu	Tyr Cys Glu Ser Gln	Met Gly Gln Gly Thr	Arg
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Pro Ser Pro Thr	Pro Val Thr Pro Arg	Pro Pro Arg Ser Leu	Thr
	455	460	465
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Gln Arg Tyr Leu	Gln Gly Ser Ser Val	Gln Leu Arg Ser Leu	Arg
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Arg Pro Asn Ala	Thr Tyr Ser Val Cys	Val Met Pro Leu Gly	Pro
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Pro Pro Ala Val	His Ser Asn His Ala	Pro Val Thr Gln Ala	Arg
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Glu Gly Asn Leu	Pro Leu Leu Ile Ala	Pro Ala Leu Ala Ala	Val
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Arg Gly Arg Ala	Met Ala Ala Ala Ala	Gln Asp Lys Gly Gln	Val
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Gly Pro Gly Ala	Gly Pro Leu Glu Leu	Glu Gly Val Lys Val	Pro
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<211> 811

<212> PRT

<213> Homo sapiens

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			20						25					30
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Gly	Ala	Lys	Ile	Gln	Lys	Ser	Asp	Phe	Gln	Lys	Ile	Ala	His	Leu	
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His	Leu	Asn	Thr	Val	Phe	Leu	Gly	Phe	Arg	Thr	Leu	Pro	His	Tyr	
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Glu	Glu	Gly	Ser	Leu	Pro	Ile	Leu	Asn	Thr	Thr	Lys	Leu	His	Ile	
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Val	Leu	Pro	Met	Asp	Thr	Asn	Phe	Trp	Val	Leu	Leu	Arg	Asp	Gly	
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Val	Glu	His	Phe	Gln	Ile	Arg	Asn	Val	Thr	Phe	Gly	Gly	Lys	Ala	
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Tyr	Leu	Asp	His	Asn	Ser	Phe	Asp	Tyr	Ser	Asn	Thr	Val	Met	Arg	
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Thr	Ile	Lys	Leu	Glu	His	Val	His	Phe	Arg	Val	Phe	Tyr	Ile	Gln	
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Gln	Asp	Lys	Ile	Tyr	Leu	Leu	Leu	Thr	Lys	Met	Asp	Ile	Glu	Asn	
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Thr	Asp	Glu	Leu	Phe	Lys	Arg	Thr	Ile	Gln	Leu	Pro	His	Leu	Lys	
				365					370					375	
Thr	Leu	Ile	Leu	Asn	Gly	Asn	Lys	Leu	Glu	Thr	Leu	Ser	Leu	Val	
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Ser	Cys	Phe	Ala	Asn	Asn	Thr	Pro	Leu	Glu	His	Leu	Asp	Leu	Ser	
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Gln	Asn	Leu	Leu	Gln	His	Lys	Asn	Asp	Glu	Asn	Cys	Ser	Trp	Pro	410	415	420
Glu	Thr	Val	Val	Asn	Met	Asn	Leu	Ser	Tyr	Asn	Lys	Leu	Ser	Asp	425	430	435
Ser	Val	Phe	Arg	Cys	Leu	Pro	Lys	Ser	Ile	Gln	Ile	Leu	Asp	Leu	440	445	450
Asn	Asn	Asn	Gln	Ile	Gln	Thr	Val	Pro	Lys	Glu	Thr	Ile	His	Leu	455	460	465
Met	Ala	Leu	Arg	Glu	Leu	Asn	Ile	Ala	Phe	Asn	Phe	Leu	Thr	Asp	470	475	480
Leu	Pro	Gly	Cys	Ser	His	Phe	Ser	Arg	Leu	Ser	Val	Leu	Asn	Ile	485	490	495
Glu	Met	Asn	Phe	Ile	Leu	Ser	Pro	Ser	Leu	Asp	Phe	Val	Gln	Ser	500	505	510
Cys	Gln	Glu	Val	Lys	Thr	Leu	Asn	Ala	Gly	Arg	Asn	Pro	Phe	Arg	515	520	525
Cys	Thr	Cys	Glu	Leu	Lys	Asn	Phe	Ile	Gln	Leu	Glu	Thr	Tyr	Ser	530	535	540
Glu	Val	Met	Met	Val	Gly	Trp	Ser	Asp	Ser	Tyr	Thr	Cys	Glu	Tyr	545	550	555
Pro	Leu	Asn	Leu	Arg	Gly	Thr	Arg	Leu	Lys	Asp	Val	His	Leu	His	560	565	570
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Thr	Trp	His	Arg	Val	Arg	Lys	Thr	Thr	Gln	Glu	Gln	Leu	Lys	Arg	620	625	630
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Gly	Ser	Ile	Leu	Ile	Cys	Leu	Tyr	Glu	Ser	Tyr	Phe	Asp	Pro	Gly	665	670	675
Lys	Ser	Ile	Ser	Glu	Asn	Ile	Val	Ser	Phe	Ile	Glu	Lys	Ser	Tyr	680	685	690
Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn	Glu	Trp	695	700	705
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Tyr	Cys	Ile	Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu
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Lys	Lys	Ala	Tyr	Leu	Glu	Trp	Pro	Lys	Asp	Arg	Arg	Lys	Cys	Gly
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 gttcagaaaa ggagagagag gctgagatca ttcaggagt ttgttgggcag 3250  
 caagcatgga gtttcttgca caaattctgg gtccataaac aacccccaaa 3300

gtccctgctg atccagtagc cctggagggtt ccccaggtag ggagagccag 3350  
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 cagtttggga agaattattg aattatcttg caagaaaaaa gtatgtctca 3650  
 ctttttgta atgttgctgc ctcatcgacc tgggaaaaat gaaaaaaaaa 3700  
 aataagcaa atggtaagac ccttaaaaaa aaaaaaaaaa aaaaaaaaaa 3750  
 aaaaaaaaaa aaaaaaaaaa aa 3772

<210> 62

<211> 756

<212> PRT

<213> Homo sapiens

<400> 62

Met	Ser	Arg	Pro	Gly	Thr	Ala	Thr	Pro	Ala	Leu	Ala	Leu	Val	Leu	1	5	10	15
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Glu	Asp	Pro	Asp	Tyr	Tyr	Gly	Gln	Glu	Ile	Trp	Ser	Arg	Glu	Pro	35	40	45	
Tyr	Tyr	Ala	Arg	Pro	Glu	Pro	Glu	Leu	Glu	Thr	Phe	Ser	Pro	Pro	50	55	60	
Leu	Pro	Ala	Gly	Pro	Gly	Glu	Glu	Trp	Glu	Arg	Arg	Pro	Gln	Glu	65	70	75	
Pro	Arg	Pro	Pro	Lys	Arg	Ala	Thr	Lys	Pro	Lys	Lys	Ala	Pro	Lys	80	85	90	
Arg	Glu	Lys	Ser	Ala	Pro	Glu	Pro	Pro	Pro	Pro	Gly	Lys	His	Ser	95	100	105	
Asn	Lys	Lys	Val	Met	Arg	Thr	Lys	Ser	Ser	Glu	Lys	Ala	Ala	Asn	110	115	120	
Asp	Asp	His	Ser	Val	Arg	Val	Ala	Arg	Glu	Asp	Val	Arg	Glu	Ser	125	130	135	
Cys	Pro	Pro	Leu	Gly	Leu	Glu	Thr	Leu	Lys	Ile	Thr	Asp	Phe	Gln	140	145	150	
Leu	His	Ala	Ser	Thr	Val	Lys	Arg	Tyr	Gly	Leu	Gly	Ala	His	Arg	155	160	165	
Gly	Arg	Leu	Asn	Ile	Gln	Ala	Gly	Ile	Asn	Glu	Asn	Asp	Phe	Tyr	170	175	180	
Asp	Gly	Ala	Trp	Cys	Ala	Gly	Arg	Asn	Asp	Leu	Gln	Gln	Trp	Ile				

185										190				195			
Glu	Val	Asp	Ala	Arg	Arg	Leu	Thr	Arg	Phe	Thr	Gly	Val	Ile	Thr			
				200					205					210			
Gln	Gly	Arg	Asn	Ser	Leu	Trp	Leu	Ser	Asp	Trp	Val	Thr	Ser	Tyr			
				215					220					225			
Lys	Val	Met	Val	Ser	Asn	Asp	Ser	His	Thr	Trp	Val	Thr	Val	Lys			
				230					235					240			
Asn	Gly	Ser	Gly	Asp	Met	Ile	Phe	Glu	Gly	Asn	Ser	Glu	Lys	Glu			
				245					250					255			
Ile	Pro	Val	Leu	Asn	Glu	Leu	Pro	Val	Pro	Met	Val	Ala	Arg	Tyr			
				260					265					270			
Ile	Arg	Ile	Asn	Pro	Gln	Ser	Trp	Phe	Asp	Asn	Gly	Ser	Ile	Cys			
				275					280					285			
Met	Arg	Met	Glu	Ile	Leu	Gly	Cys	Pro	Leu	Pro	Asp	Pro	Asn	Asn			
				290					295					300			
Tyr	Tyr	His	Arg	Arg	Asn	Glu	Met	Thr	Thr	Thr	Asp	Asp	Leu	Asp			
				305					310					315			
Phe	Lys	His	His	Asn	Tyr	Lys	Glu	Met	Arg	Gln	Leu	Met	Lys	Val			
				320					325					330			
Val	Asn	Glu	Met	Cys	Pro	Asn	Ile	Thr	Arg	Ile	Tyr	Asn	Ile	Gly			
				335					340					345			
Lys	Ser	His	Gln	Gly	Leu	Lys	Leu	Tyr	Ala	Val	Glu	Ile	Ser	Asp			
				350					355					360			
His	Pro	Gly	Glu	His	Glu	Val	Gly	Glu	Pro	Glu	Phe	His	Tyr	Ile			
				365					370					375			
Ala	Gly	Ala	His	Gly	Asn	Glu	Val	Leu	Gly	Arg	Glu	Leu	Leu	Leu			
				380					385					390			
Leu	Leu	Val	Gln	Phe	Val	Cys	Gln	Glu	Tyr	Leu	Ala	Arg	Asn	Ala			
				395					400					405			
Arg	Ile	Val	His	Leu	Val	Glu	Glu	Thr	Arg	Ile	His	Val	Leu	Pro			
				410					415					420			
Ser	Leu	Asn	Pro	Asp	Gly	Tyr	Glu	Lys	Ala	Tyr	Glu	Gly	Gly	Ser			
				425					430					435			
Glu	Leu	Gly	Gly	Trp	Ser	Leu	Gly	Arg	Trp	Thr	His	Asp	Gly	Ile			
				440					445					450			
Asp	Ile	Asn	Asn	Asn	Phe	Pro	Asp	Leu	Asn	Thr	Leu	Leu	Trp	Glu			
				455					460					465			
Ala	Glu	Asp	Arg	Gln	Asn	Val	Pro	Arg	Lys	Val	Pro	Asn	His	Tyr			
				470					475					480			
Ile	Ala	Ile	Pro	Glu	Trp	Phe	Leu	Ser	Glu	Asn	Ala	Thr	Val	Ala			
				485					490					495			
Ala	Glu	Thr	Arg	Ala	Val	Ile	Ala	Trp	Met	Glu	Lys	Ile	Pro	Phe			

500	505	510
Val Leu Gly Gly Asn Leu Gln Gly Gly	Glu Leu Val Val Ala Tyr	
515	520	525
Pro Tyr Asp Leu Val Arg Ser Pro Trp	Lys Thr Gln Glu His Thr	
530	535	540
Pro Thr Pro Asp Asp His Val Phe Arg	Trp Leu Ala Tyr Ser Tyr	
545	550	555
Ala Ser Thr His Arg Leu Met Thr Asp	Ala Arg Arg Arg Val Cys	
560	565	570
His Thr Glu Asp Phe Gln Lys Glu Glu	Gly Thr Val Asn Gly Ala	
575	580	585
Ser Trp His Thr Val Ala Gly Ser Leu	Asn Asp Phe Ser Tyr Leu	
590	595	600
His Thr Asn Cys Phe Glu Leu Ser Ile	Tyr Val Gly Cys Asp Lys	
605	610	615
Tyr Pro His Glu Ser Gln Leu Pro Glu	Glu Trp Glu Asn Asn Arg	
620	625	630
Glu Ser Leu Ile Val Phe Met Glu Gln	Val His Arg Gly Ile Lys	
635	640	645
Gly Leu Val Arg Asp Ser His Gly Lys	Gly Ile Pro Asn Ala Ile	
650	655	660
Ile Ser Val Glu Gly Ile Asn His Asp	Ile Arg Thr Ala Asn Asp	
665	670	675
Gly Asp Tyr Trp Arg Leu Leu Asn Pro	Gly Glu Tyr Val Val Thr	
680	685	690
Ala Lys Ala Glu Gly Phe Thr Ala Ser	Thr Lys Asn Cys Met Val	
695	700	705
Gly Tyr Asp Met Gly Ala Thr Arg Cys	Asp Phe Thr Leu Ser Lys	
710	715	720
Thr Asn Met Ala Arg Ile Arg Glu Ile	Met Glu Lys Phe Gly Lys	
725	730	735
Gln Pro Val Ser Leu Pro Ala Arg Arg	Leu Lys Leu Arg Gly Arg	
740	745	750
Lys Arg Arg Gln Arg Gly		
755		

<210> 63

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 63

gttctcaatg agctacccgt cccc 24

<210> 64  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 64  
cgcgatgtag tggaactcgg gctc 24

<210> 65  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 65  
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<210> 66  
<211> 2854  
<212> DNA  
<213> Homo sapiens

<400> 66  
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cccagccccg gcttcagctc tttcccaggt gttgactcca gctccagctt 150  
cagctccagc tccaggtcgg gctccagctc cagccgcagc ttaggcagcg 200  
gaggttctgt gtcccagttg ttttccaatt tcacoggctc cgtggatgac 250  
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ggacagagtg gaacgcttgg aattcacagc tcatgttctt tctcagaagt 350  
ttgagaaaga actttctaaa gtgagggaat atgtccaatt aattagtgtg 400  
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gccgagaaat cgtggctctg aagaocaaagc tgaaagagtg tgaggcctct 700  
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 ggtacagcag tttacaacaa caacatgtac gtcaacatgt acaacaccgg 1050  
 gaatattgcc agagttaacc tgaccaccaa cacgattgct gtgactcaaa 1100  
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 ccacacttca ggtgctaaac acttgggtata ccaagcagta taaaccatct 1300  
 gcttctaacg ccttcatggg atgtgggggt ctgtatgcc cccgtactat 1350  
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aaaataaatg attaaaatgt gctttgaaaa aaaaaaaaaa aaaaaaaaaa 2850  
aaaa 2854

<210> 67

<211> 510

<212> PRT

<213> Homo sapiens

<400> 67

Met	Arg	Pro	Gly	Leu	Ser	Phe	Leu	Leu	Ala	Leu	Leu	Phe	Phe	Leu	1	5	10	15
Gly	Gln	Ala	Ala	Gly	Asp	Leu	Gly	Asp	Val	Gly	Pro	Pro	Ile	Pro	20	25	30	
Ser	Pro	Gly	Phe	Ser	Ser	Phe	Pro	Gly	Val	Asp	Ser	Ser	Ser	Ser	35	40	45	
Phe	Ser	Ser	Ser	Ser	Arg	Ser	Gly	Ser	Ser	Ser	Arg	Ser	Leu	50	55	60		
Gly	Ser	Gly	Gly	Ser	Val	Ser	Gln	Leu	Phe	Ser	Asn	Phe	Thr	Gly	65	70	75	
Ser	Val	Asp	Asp	Arg	Gly	Thr	Cys	Gln	Cys	Ser	Val	Ser	Leu	Pro	80	85	90	
Asp	Thr	Thr	Phe	Pro	Val	Asp	Arg	Val	Glu	Arg	Leu	Glu	Phe	Thr	95	100	105	
Ala	His	Val	Leu	Ser	Gln	Lys	Phe	Glu	Lys	Glu	Leu	Ser	Lys	Val	110	115	120	
Arg	Glu	Tyr	Val	Gln	Leu	Ile	Ser	Val	Tyr	Glu	Lys	Lys	Leu	Leu	125	130	135	
Asn	Leu	Thr	Val	Arg	Ile	Asp	Ile	Met	Glu	Lys	Asp	Thr	Ile	Ser	140	145	150	
Tyr	Thr	Glu	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Val	Glu	Val	Lys	Glu	155	160	165	
Met	Glu	Lys	Leu	Val	Ile	Gln	Leu	Lys	Glu	Ser	Phe	Gly	Gly	Ser	170	175	180	
Ser	Glu	Ile	Val	Asp	Gln	Leu	Glu	Val	Glu	Ile	Arg	Asn	Met	Thr	185	190	195	
Leu	Leu	Val	Glu	Lys	Leu	Glu	Thr	Leu	Asp	Lys	Asn	Asn	Val	Leu	200	205	210	

Ala	Ile	Arg	Arg	Glu	Ile	Val	Ala	Leu	Lys	Thr	Lys	Leu	Lys	Glu	215	220	225
Cys	Glu	Ala	Ser	Lys	Asp	Gln	Asn	Thr	Pro	Val	Val	His	Pro	Pro	230	235	240
Pro	Thr	Pro	Gly	Ser	Cys	Gly	His	Gly	Gly	Val	Val	Asn	Ile	Ser	245	250	255
Lys	Pro	Ser	Val	Val	Gln	Leu	Asn	Trp	Arg	Gly	Phe	Ser	Tyr	Leu	260	265	270
Tyr	Gly	Ala	Trp	Gly	Arg	Asp	Tyr	Ser	Pro	Gln	His	Pro	Asn	Lys	275	280	285
Gly	Leu	Tyr	Trp	Val	Ala	Pro	Leu	Asn	Thr	Asp	Gly	Arg	Leu	Leu	290	295	300
Glu	Tyr	Tyr	Arg	Leu	Tyr	Asn	Thr	Leu	Asp	Asp	Leu	Leu	Leu	Tyr	305	310	315
Ile	Asn	Ala	Arg	Glu	Leu	Arg	Ile	Thr	Tyr	Gly	Gln	Gly	Ser	Gly	320	325	330
Thr	Ala	Val	Tyr	Asn	Asn	Asn	Met	Tyr	Val	Asn	Met	Tyr	Asn	Thr	335	340	345
Gly	Asn	Ile	Ala	Arg	Val	Asn	Leu	Thr	Thr	Asn	Thr	Ile	Ala	Val	350	355	360
Thr	Gln	Thr	Leu	Pro	Asn	Ala	Ala	Tyr	Asn	Asn	Arg	Phe	Ser	Tyr	365	370	375
Ala	Asn	Val	Ala	Trp	Gln	Asp	Ile	Asp	Phe	Ala	Val	Asp	Glu	Asn	380	385	390
Gly	Leu	Trp	Val	Ile	Tyr	Ser	Thr	Glu	Ala	Ser	Thr	Gly	Asn	Met	395	400	405
Val	Ile	Ser	Lys	Leu	Asn	Asp	Thr	Thr	Leu	Gln	Val	Leu	Asn	Thr	410	415	420
Trp	Tyr	Thr	Lys	Gln	Tyr	Lys	Pro	Ser	Ala	Ser	Asn	Ala	Phe	Met	425	430	435
Val	Cys	Gly	Val	Leu	Tyr	Ala	Thr	Arg	Thr	Met	Asn	Thr	Arg	Thr	440	445	450
Glu	Glu	Ile	Phe	Tyr	Tyr	Tyr	Asp	Thr	Asn	Thr	Gly	Lys	Glu	Gly	455	460	465
Lys	Leu	Asp	Ile	Val	Met	His	Lys	Met	Gln	Glu	Lys	Val	Gln	Ser	470	475	480
Ile	Asn	Tyr	Asn	Pro	Phe	Asp	Gln	Lys	Leu	Tyr	Val	Tyr	Asn	Asp	485	490	495
Gly	Tyr	Leu	Leu	Asn	Tyr	Asp	Leu	Ser	Val	Leu	Gln	Lys	Pro	Gln	500	505	510

<210> 68  
 <211> 410  
 <212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 206, 217, 387

<223> unknown base

<400> 68

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ggtgaacatc agcaaaccgt ctgtgggttca gctcaactgg agagggtttt 150  
cttatctata tgggtgcttgg ggtagggatt actctcccca gcatccaaac 200  
aaaggnatgt attggngggc gccattgaat acagatggga gactgttgga 250  
gtattataga ctgtacaacc cactggatga ttgctattg tatataaatg 300  
ctcgagagtt gcggatcacc tatggccaag gtagtgggtac agcagtttac 350  
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<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 69

agctgtgggtc atgggtgggtg ggtg 24

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ctacctgggc cataggtgat ccgc 24

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

catcagcaaa ccgtctgtgg ttcagctcaa ctggagaggg tt 42

<210> 72

<211> 3127

<212> DNA

<213> Homo sapiens

<400> 72

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tggggctgtg ctccatggcg agctggatac catgtttgtg tggaagtgcc 150  
ccgtgtttgc tatgccgatg ctgtcctagt ggaaacaact ccaactgtaac 200  
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 aaggataatc atgggttaga aggaagtgtt ttgaaagtca ctttgaaagt 2200  
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 caaaaaata tatatatatt gaaatcaagg aggcaaaatt ttgacagga 2500  
 aggaagtaac tgcaaacca ctaggcttta gtaggtactt atataaaatc 2550  
 tagtccagtt ctctcattta aaaaaatgaa gacactgaaa tacagactta 2600  
 aatagctcag atagctaatt aggaaatttc aagttggcca ataatagcat 2650  
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 ttacacctca tactgtgata attaatgtga tgtggattgc tgggtgtccag 2750  
 catgacccat aaacaggtca gaagaatgat ggaatgtttt agaataaact 2800  
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 taatgaagct tttaaaatct acaatttctt ctttaaaaat atttattaat 3000  
 gtgaatggaa tataacaatt cagcttaatt cccaacctt attctgtgtg 3050  
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 atgaattcag agaaaaaaaa aaaaaa 3127

<210> 73  
 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 73

Met	Gly	Ser	Val	Leu	Gly	Leu	Cys	Ser	Met	Ala	Ser	Trp	Ile	Pro
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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Leu	Leu	Cys	Arg	Cys	Cys	Pro
				20					25					30
Ser	Gly	Asn	Asn	Ser	Thr	Val	Thr	Arg	Leu	Ile	Tyr	Ala	Leu	Phe
				35					40					45
Leu	Leu	Val	Gly	Val	Cys	Val	Ala	Cys	Val	Met	Leu	Ile	Pro	Gly
				50					55	.				60
Met	Glu	Glu	Gln	Leu	Asn	Lys	Ile	Pro	Gly	Phe	Cys	Glu	Asn	Glu
				65					70					75
Lys	Gly	Val	Val	Pro	Cys	Asn	Ile	Leu	Val	Gly	Tyr	Lys	Ala	Val
				80					85					90
Tyr	Arg	Leu	Cys	Phe	Gly	Leu	Ala	Met	Phe	Tyr	Leu	Leu	Leu	Ser
				95					100					105
Leu	Leu	Met	Ile	Lys	Val	Lys	Ser	Ser	Ser	Asp	Pro	Arg	Ala	Ala
				110					115					120
Val	His	Asn	Gly	Phe	Trp	Phe	Phe	Lys	Phe	Ala	Ala	Ala	Ile	Ala
				125					130					135
Ile	Ile	Ile	Gly	Ala	Phe	Phe	Ile	Pro	Glu	Gly	Thr	Phe	Thr	Thr
				140					145					150
Val	Trp	Phe	Tyr	Val	Gly	Met	Ala	Gly	Ala	Phe	Cys	Phe	Ile	Leu
				155					160					165
Ile	Gln	Leu	Val	Leu	Leu	Ile	Asp	Phe	Ala	His	Ser	Trp	Asn	Glu
				170					175					180
Ser	Trp	Val	Glu	Lys	Met	Glu	Glu	Gly	Asn	Ser	Arg	Cys	Trp	Tyr
				185					190					195
Ala	Ala	Leu	Leu	Ser	Ala	Thr	Ala	Leu	Asn	Tyr	Leu	Leu	Ser	Leu
				200					205					210
Val	Ala	Ile	Val	Leu	Phe	Phe	Val	Tyr	Tyr	Thr	His	Pro	Ala	Ser
				215					220					225
Cys	Ser	Glu	Asn	Lys	Ala	Phe	Ile	Ser	Val	Asn	Met	Leu	Leu	Cys
				230					235					240
Val	Gly	Ala	Ser	Val	Met	Ser	Ile	Leu	Pro	Lys	Ile	Gln	Glu	Ser
				245					250					255
Gln	Pro	Arg	Ser	Gly	Leu	Leu	Gln	Ser	Ser	Val	Ile	Thr	Val	Tyr
				260					265					270
Thr	Met	Tyr	Leu	Thr	Trp	Ser	Ala	Met	Thr	Asn	Glu	Pro	Glu	Thr
				275					280					285

Asn	Cys	Asn	Pro	Ser	Leu	Leu	Ser	Ile	Ile	Gly	Tyr	Asn	Thr	Thr	290	295	300
Ser	Thr	Val	Pro	Lys	Glu	Gly	Gln	Ser	Val	Gln	Trp	Trp	His	Ala	305	310	315
Gln	Gly	Ile	Ile	Gly	Leu	Ile	Leu	Phe	Leu	Leu	Cys	Val	Phe	Tyr	320	325	330
Ser	Ser	Ile	Arg	Thr	Ser	Asn	Asn	Ser	Gln	Val	Asn	Lys	Leu	Thr	335	340	345
Leu	Thr	Ser	Asp	Glu	Ser	Thr	Leu	Ile	Glu	Asp	Gly	Gly	Ala	Arg	350	355	360
Ser	Asp	Gly	Ser	Leu	Glu	Asp	Gly	Asp	Asp	Val	His	Arg	Ala	Val	365	370	375
Asp	Asn	Glu	Arg	Asp	Gly	Val	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	His	380	385	390
Phe	Met	Leu	Phe	Leu	Ala	Ser	Leu	Tyr	Ile	Met	Met	Thr	Leu	Thr	395	400	405
Asn	Trp	Ser	Arg	Tyr	Glu	Pro	Ser	Arg	Glu	Met	Lys	Ser	Gln	Trp	410	415	420
Thr	Ala	Val	Trp	Val	Lys	Ile	Ser	Ser	Ser	Trp	Ile	Gly	Ile	Val	425	430	435
Leu	Tyr	Val	Trp	Thr	Leu	Val	Ala	Pro	Leu	Val	Leu	Thr	Asn	Arg	440	445	450

Asp Phe Asp

<210> 74  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 48, 163  
 <223> unknown base

<400> 74  
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 cgttgtggag atggggagcg tccctggggc tgtgtccat ggcgagctgg 100  
 ataccatgtt tgttgtggaag tgccccgtgt ttgctatgcc gatgctgtcc 150  
 tagtggaac aantccactg taactagatt gatctatgca cttttcttgc 200  
 ttgttgagat atgtgtagct tgtgtaatgt tgataccagg aatggaagaa 250  
 caactgaata agattcctgg attttgtgag aatgagaaag gtgttgtccc 300  
 ttgtaacatt ttggttggt ataaagctgt atatcgtttg tgctttggtt 350  
 tggctatgtt ctatcttctt ctctctttac taatgatcaa agtgaagagt 400

agcagtgatc ctagagctgc agtgcacaat ggatttttgt tctttaaatt 450  
tgctgcagca attgcaatta ttattggggc 480

<210> 75  
<211> 438  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 65, 92, 121, 142, 154, 170, 293, 315, 323  
<223> unknown base

<400> 75  
gttattgtga actttgtgga gatgggaggt cntggggctg tgttccatgg 50  
cgagctggat accangtttg tgtggaagtg ccccggtgtt gntatgccga 100  
tgctgtccta gtggaacaaa ntccactgta attagattga tntatgcact 150  
tttnttgctt gttggagtan gtgtagcttg tgtaatgttg ataccaggaa 200  
tggaagaaca actgaataag attcctggat tttgtgagaa tgagaaaggt 250  
gttgtccctt gtaacatttt ggttggctat aaagctgtat atngtttgtg 300  
ctttggtttg gctangttct atnttcttct ctctttacta atgatcaaag 350  
tgaagagtag cagtgatcct agagctgcag tgcacaatgg attttggttt 400  
tttaaatttg ctgcagcaat tgcaattatt attggggc 438

<210> 76  
<211> 473  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 48  
<223> unknown base

<400> 76  
aagaagctgt ctccatcttg tctgtatccg ctgctcttgt gaacgttntg 50  
gagatgggga gcgtccttgg ggttgtgctc catggcgagc tggataccat 100  
gtttgtgtgg aagtgcctcg tgtttgctat gccgatgctg tcctagtggg 150  
aacaactcca ctgtaactag attgatctat gcacttttct tgcttggttg 200  
agtatgtgta gcttgtgtaa tgttgatacc aggaatggaa gaacaactga 250  
ataagattcc tggattttgt gagaatgaga aaggtgttgt cccttgtaac 300  
attttggttg gctataaagc tgtatatcgt ttgtgctttg gtttggctat 350  
gttctatctt cttctctctt tactaatgat caaagtgaag agtagcagt 400  
atcctagagc tgcagtgcac aatggatttt ggttctttaa atttgctgca 450  
gcaattgcaa ttattatttg ggc 473

<210> 77  
<211> 666  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 21, 111  
<223> unknown base

<400> 77  
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actttttcct tgcttggttg agtatgtgta gctttgtgta atgttggtcc 100  
caggattgga ngaacaactg aataagattc ctggattttt gtgagaatga 150  
gaaaggtggt gtcccccttg aacatttttg gttggctata aagctgtata 200  
tcgtttgtgc tttggtttgg ctatgttcta tcttcttctc tctttactaa 250  
tgatcaaagt gaagagtagc agtgatccta gagctgcagt gcacaatgga 300  
ttttggttct ttaaatttgc tgcagcaatt gcaattatta ttggggcatt 350  
cttcattcca gaaggaaact ttacaactgt gtggttttat gtaggcatgg 400  
cagggtgcctt ttgtttcatc ctcatacaac tagtcttact tattgatttt 450  
gcacattcat ggaatgaatc gtgggttgaa aaaatggaag aagggaactc 500  
gagatgttgg tatgcagcct tgttatcagc tacagctctg aattatctgc 550  
tgtctttagt tgctatcgtc ctgttctttg tctactacac tcatccagcc 600  
agttgttcag aaaacaaggc gttcatcagt gtcaacatgc tcctctgcgt 650  
tggtgcttct gtaatg 666

<210> 78  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 78  
atgtttgtgt ggaagtgcc cg 22

<210> 79  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 79  
gtcaacatgc tcctctgc 18

<210> 80  
<211> 26

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 80  
aatccattgt gcactgcagc tctagg 26

<210> 81  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 81  
gagcatgccca ccaactggact gac 23

<210> 82  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 82  
gccgatgctg tcctagtggg aacaactcca ctgtaactag attgatctat 50  
gcac 54

<210> 83  
<211> 3906  
<212> DNA  
<213> Homo sapiens

<400> 83  
ctcgggcgcg cacaggcagc tcggtttgcc ctgcgattga gctgcgggtc 50  
gcgggcggcg ccggcctctc caatggcaaa tgtgtgtggc tggaggcgag 100  
cgcgaggctt tcggcaaagg cagtcgagtg tttgcagacc ggggcgagtc 150  
ctgtgaaagc agataaaaga aacatttat taacgtgtca ttacgagggg 200  
agcgcccggc cggggctgtc gactccccg cggaacattt ggctccctcc 250  
agctccgaga gaggagaaga agaaagcgga aaagaggcag attcacgtcg 300  
tttccagcca agtggacctg atcgatggcc ctctgaatt tatcacgata 350  
tttgatttat tagcgatgcc ccttggtttg tgtgttacgc acacacacgt 400  
gcacacaagg ctctggctcg cttccctccc tcgtttccag ctctgggcg 450  
aatcccacat ctgtttcaac tctccgccga gggcgagcag gagcgagagt 500  
gtgtcgaatc tgcgagtga gaggacgag ggaaaagaaa caaagccaca 550  
gacgcaactt gagactcccc catccccaaa gaagcaccag atcagcaaaa 600

aaagaagatg ggccccccga gcctcgtgct gtgcttgctg tccgcaactg 650  
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 ggtgctgacg gacgaccagg atgtggagct gggttccatg caggatgatga 800  
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 ttcgtgacca caccatgtg ctgcctctca cgctcctcca tcctcactgg 900  
 caagtacgtc cacaaccaca acacctacac caacaatgag aactgctcct 950  
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 aagcaaggct ccgactactc caaggattac ctacacagacc tcatcaccaa 1200  
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 gccccacaat attcagcct cttcccaaac gcattctcagc acatcacgcc 1350  
 gagctacaac tacgcgcccc acccggacaa aactggatc atgcgctaca 1400  
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 aaacctggt tgcctctgaa gaaactgcct tcattgtata tatgtgacta 3800

tttacatgta atcaacatgg gaacttttag gggaacctaa taagaaatcc 3850  
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 gaaaaa 3906

<210> 84  
 <211> 867  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 Phe Ser Leu Leu Gly Gly Ser Ser Ala Phe Leu Ser His His Arg  
 20 25 30  
 Leu Lys Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn  
 35 40 45  
 Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser  
 50 55 60  
 Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly  
 65 70 75  
 Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro  
 80 85 90  
 Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn  
 95 100 105  
 Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala  
 110 115 120  
 Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly  
 125 130 135  
 Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly  
 140 145 150  
 Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys  
 155 160 165  
 Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys  
 170 175 180  
 Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu  
 185 190 195  
 Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met  
 200 205 210  
 Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro  
 215 220 225  
 His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro  
 230 235 240  
 Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn  
 245 250 255

Pro	Asp	Lys	His	Trp	Ile	Met	Arg	Tyr	Thr	Gly	Pro	Met	Lys	Pro	260	265	270
Ile	His	Met	Glu	Phe	Thr	Asn	Met	Leu	Gln	Arg	Lys	Arg	Leu	Gln	275	280	285
Thr	Leu	Met	Ser	Val	Asp	Asp	Ser	Met	Glu	Thr	Ile	Tyr	Asn	Met	290	295	300
Leu	Val	Glu	Thr	Gly	Glu	Leu	Asp	Asn	Thr	Tyr	Ile	Val	Tyr	Thr	305	310	315
Ala	Asp	His	Gly	Tyr	His	Ile	Gly	Gln	Phe	Gly	Leu	Val	Lys	Gly	320	325	330
Lys	Ser	Met	Pro	Tyr	Glu	Phe	Asp	Ile	Arg	Val	Pro	Phe	Tyr	Val	335	340	345
Arg	Gly	Pro	Asn	Val	Glu	Ala	Gly	Cys	Leu	Asn	Pro	His	Ile	Val	350	355	360
Leu	Asn	Ile	Asp	Leu	Ala	Pro	Thr	Ile	Leu	Asp	Ile	Ala	Gly	Leu	365	370	375
Asp	Ile	Pro	Ala	Asp	Met	Asp	Gly	Lys	Ser	Ile	Leu	Lys	Leu	Leu	380	385	390
Asp	Thr	Glu	Arg	Pro	Val	Asn	Arg	Phe	His	Leu	Lys	Lys	Lys	Met	395	400	405
Arg	Val	Trp	Arg	Asp	Ser	Phe	Leu	Val	Glu	Arg	Gly	Lys	Leu	Leu	410	415	420
His	Lys	Arg	Asp	Asn	Asp	Lys	Val	Asp	Ala	Gln	Glu	Glu	Asn	Phe	425	430	435
Leu	Pro	Lys	Tyr	Gln	Arg	Val	Lys	Asp	Leu	Cys	Gln	Arg	Ala	Glu	440	445	450
Tyr	Gln	Thr	Ala	Cys	Glu	Gln	Leu	Gly	Gln	Lys	Trp	Gln	Cys	Val	455	460	465
Glu	Asp	Ala	Thr	Gly	Lys	Leu	Lys	Leu	His	Lys	Cys	Lys	Gly	Pro	470	475	480
Met	Arg	Leu	Gly	Gly	Ser	Arg	Ala	Leu	Ser	Asn	Leu	Val	Pro	Lys	485	490	495
Tyr	Tyr	Gly	Gln	Gly	Ser	Glu	Ala	Cys	Thr	Cys	Asp	Ser	Gly	Asp	500	505	510
Tyr	Lys	Leu	Ser	Leu	Ala	Gly	Arg	Arg	Lys	Lys	Leu	Phe	Lys	Lys	515	520	525
Lys	Tyr	Lys	Ala	Ser	Tyr	Val	Arg	Ser	Arg	Ser	Ile	Arg	Ser	Val	530	535	540
Ala	Ile	Glu	Val	Asp	Gly	Arg	Val	Tyr	His	Val	Gly	Leu	Gly	Asp	545	550	555
Ala	Ala	Gln	Pro	Arg	Asn	Leu	Thr	Lys	Arg	His	Trp	Pro	Gly	Ala	560	565	570

Pro	Glu	Asp	Gln	Asp	Asp	Lys	Asp	Gly	Gly	Asp	Phe	Ser	Gly	Thr	
				575					580					585	
Gly	Gly	Leu	Pro	Asp	Tyr	Ser	Ala	Ala	Asn	Pro	Ile	Lys	Val	Thr	
				590					595					600	
His	Arg	Cys	Tyr	Ile	Leu	Glu	Asn	Asp	Thr	Val	Gln	Cys	Asp	Leu	
				605					610					615	
Asp	Leu	Tyr	Lys	Ser	Leu	Gln	Ala	Trp	Lys	Asp	His	Lys	Leu	His	
				620					625					630	
Ile	Asp	His	Glu	Ile	Glu	Thr	Leu	Gln	Asn	Lys	Ile	Lys	Asn	Leu	
				635					640					645	
Arg	Glu	Val	Arg	Gly	His	Leu	Lys	Lys	Lys	Arg	Pro	Glu	Glu	Cys	
				650					655					660	
Asp	Cys	His	Lys	Ile	Ser	Tyr	His	Thr	Gln	His	Lys	Gly	Arg	Leu	
				665					670					675	
Lys	His	Arg	Gly	Ser	Ser	Leu	His	Pro	Phe	Arg	Lys	Gly	Leu	Gln	
				680					685					690	
Glu	Lys	Asp	Lys	Val	Trp	Leu	Leu	Arg	Glu	Gln	Lys	Arg	Lys	Lys	
				695					700					705	
Lys	Leu	Arg	Lys	Leu	Leu	Lys	Arg	Leu	Gln	Asn	Asn	Asp	Thr	Cys	
				710					715					720	
Ser	Met	Pro	Gly	Leu	Thr	Cys	Phe	Thr	His	Asp	Asn	Gln	His	Trp	
				725					730					735	
Gln	Thr	Ala	Pro	Phe	Trp	Thr	Leu	Gly	Pro	Phe	Cys	Ala	Cys	Thr	
				740					745					750	
Ser	Ala	Asn	Asn	Asn	Thr	Tyr	Trp	Cys	Met	Arg	Thr	Ile	Asn	Glu	
				755					760					765	
Thr	His	Asn	Phe	Leu	Phe	Cys	Glu	Phe	Ala	Thr	Gly	Phe	Leu	Glu	
				770					775					780	
Tyr	Phe	Asp	Leu	Asn	Thr	Asp	Pro	Tyr	Gln	Leu	Met	Asn	Ala	Val	
				785					790					795	
Asn	Thr	Leu	Asp	Arg	Asp	Val	Leu	Asn	Gln	Leu	His	Val	Gln	Leu	
				800					805					810	
Met	Glu	Leu	Arg	Ser	Cys	Lys	Gly	Tyr	Lys	Gln	Cys	Asn	Pro	Arg	
				815					820					825	
Thr	Arg	Asn	Met	Asp	Leu	Asp	Gly	Gly	Ser	Tyr	Glu	Gln	Tyr	Arg	
				830					835					840	
Gln	Phe	Gln	Arg	Arg	Lys	Trp	Pro	Glu	Met	Lys	Arg	Pro	Ser	Ser	
				845					850					855	
Lys	Ser	Leu	Gly	Gln	Leu	Trp	Glu	Gly	Trp	Glu	Gly				
				860					865						

<210> 85  
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 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 85

gaagccggct gtctgaatc 19

<210> 86

<211> 18

<212> DNA

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<210> 87

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 87

aagggcctgc aagagaag 18

<210> 88

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 88

cactgggaca actgtggg 18

<210> 89

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 89

cagaggcaac gtggagag 18

<210> 90

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 90

aagtattgtc atacagtgtt c 21

<210> 91  
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<212> DNA  
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<220>  
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<400> 91  
tagtacttgg gcacgaggtt ggag 24

<210> 92  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
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<210> 93  
<211> 45  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
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<210> 94  
<211> 971  
<212> DNA  
<213> Homo sapiens

<400> 94  
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tgggcctcct ggggagcaca gccctcgtgg gatggatcac aggtgctgct 150  
gtggcgggtcc tgetgctgct gctgctgctg gccacctgcc ttttccacgg 200  
acggcaggac tgtgacgtgg agaggaaccg tacagctgca gggggaaacc 250  
gagtccgccc ggcccagcct tggcccttcc ggcggcgggg ccacctggga 300  
atcttttcacc atcacgctca tcctggccac gtatctcatg tgccgaatgt 350  
gggcctccac caccaccacc acccccgcca caccctcac cacctccacc 400  
accaccacca cccccaccgc caccatcccc gccacgctcg ctgaggctgc 450  
tgtogccggt gcctgtggac agcagctgcc cctgccctcc catctgttcc 500  
caggacaagt ggaccccatg tttccatgtg gaaggatgca tctctggggt 550  
gaacgagggg aacaatagac tggggcttgc tccagctgca tttgcatggc 600

atgccccagt gtactatggc agcagagaat ggaggaacac tgggtctgca 650  
 gtgctgaagg gtttggggag tggagagcaa ggggtgctctt tcggggctgg 700  
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 gtgtcttggc agagccagca cacaagtgga tgtgaagtgc ccgtcttgac 800  
 ctctcatca ggctgctgca ggctctggc gggcagggca ctgggagagg 850  
 ccctgagaat gtccttttgg tttggagaag gcagtgtgag gctgcacagt 900  
 caattcatcg gtgccttagt ccaagaaaat aaaaaccact aagaagcttt 950  
 aaaaaaaaaa aaaaaaaaaa a 971

<210> 95  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 95  
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 20 25 30  
 Cys Leu Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg  
 35 40 45  
 Thr Ala Ala Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro  
 50 55 60  
 Phe Arg Arg Arg Gly His Leu Gly Ile Phe His His His Arg His  
 65 70 75  
 Pro Gly His Val Ser His Val Pro Asn Val Gly Leu His His His  
 80 85 90  
 His His Pro Arg His Thr Pro His His Leu His His His His His  
 95 100 105  
 Pro His Arg His His Pro Arg His Ala Arg  
 110 115

<210> 96  
 <211> 1312  
 <212> DNA  
 <213> Homo sapiens

<400> 96  
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 gctgacgctg ctggcctttg ccgggtactc agggctactg gctgggggtgg 150  
 aagtgagtgc tgggtcaccc cccatccgca acgtcactgt ggcctacaag 200  
 ttccacatgg ggctctatgg tgagactggg cggcttttca ctgagagctg 250  
 cagcatctct cccaagctcc gctccatcgc tgtctactat gacaaccccc 300

acatggtgcc ccoctgataag tgccgatgtg ccgtgggcag catcctgagt 350  
 gaaggtgagg aatcgccctc ccoctgagctc atcgacctct accagaaatt 400  
 tggcttcaag gtgtttctct tcccggcacc cagccatgtg gtgacagcca 450  
 ccttccccta caccaccatt ctgtccatct ggctggctac ccgccgtgtc 500  
 catcctgcct tggacaccta catcaaggag cggaagctgt gtgcctatcc 550  
 tcggctggag atctaccagg aagaccagat ccatttcatg tgcccactgg 600  
 cacggcaggg agaattctat gtgcctgaga tgaaggagac agagtggaaa 650  
 tggcgggggc ttgtggaggc cattgacacc caggtggatg gcacaggagc 700  
 tgacacaatg agtgacacga gttctgtaa gcttggaaagt agccctggca 750  
 gccgggagac ttcagctgcc aactgtcac ctggggcgag cagccgtggc 800  
 tgggatgacg gtgacacccg cagcgagcac agctacagcg agtcaggtgc 850  
 cagcggctcc tcttttgagg agctggactt ggagggcgag gggcccttag 900  
 gggagtcacg gctggaccct gggactgagc ccctggggac taccaagtgg 950  
 ctctgggagc cactgcccc tgagaagggc aaggagtaac ccatggcctg 1000  
 caccctctg cagtgcagtt gctgaggaac tgagcagact ctccagcaga 1050  
 ctctccagcc ctcttctctc ttcctctggg ggaggagggg ttcttgaggg 1100  
 acctgacttc cctgctcca ggcctcttgc taagccttct cctcactgcc 1150  
 ctttaggctc ccagggccag aggagccagg gactattttc tgcaccagcc 1200  
 ccagggctg ccgccctgt tgtgtctttt tttcagactc acagtggagc 1250  
 ttccaggacc cagaataaag ccaatgattt acttgtttca cctggaaaaa 1300  
 aaaaaaaaaa aa 1312

<210> 97  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 97  
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 20 25 30  
 Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn  
 35 40 45  
 Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr  
 50 55 60  
 Gly Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg  
 65 70 75

Ser	Ile	Ala	Val	Tyr	Tyr	Asp	Asn	Pro	His	Met	Val	Pro	Pro	Asp	80	85	90
Lys	Cys	Arg	Cys	Ala	Val	Gly	Ser	Ile	Leu	Ser	Glu	Gly	Glu	Glu	95	100	105
Ser	Pro	Ser	Pro	Glu	Leu	Ile	Asp	Leu	Tyr	Gln	Lys	Phe	Gly	Phe	110	115	120
Lys	Val	Phe	Ser	Phe	Pro	Ala	Pro	Ser	His	Val	Val	Thr	Ala	Thr	125	130	135
Phe	Pro	Tyr	Thr	Thr	Ile	Leu	Ser	Ile	Trp	Leu	Ala	Thr	Arg	Arg	140	145	150
Val	His	Pro	Ala	Leu	Asp	Thr	Tyr	Ile	Lys	Glu	Arg	Lys	Leu	Cys	155	160	165
Ala	Tyr	Pro	Arg	Leu	Glu	Ile	Tyr	Gln	Glu	Asp	Gln	Ile	His	Phe	170	175	180
Met	Cys	Pro	Leu	Ala	Arg	Gln	Gly	Asp	Phe	Tyr	Val	Pro	Glu	Met	185	190	195
Lys	Glu	Thr	Glu	Trp	Lys	Trp	Arg	Gly	Leu	Val	Glu	Ala	Ile	Asp	200	205	210
Thr	Gln	Val	Asp	Gly	Thr	Gly	Ala	Asp	Thr	Met	Ser	Asp	Thr	Ser	215	220	225
Ser	Val	Ser	Leu	Glu	Val	Ser	Pro	Gly	Ser	Arg	Glu	Thr	Ser	Ala	230	235	240
Ala	Thr	Leu	Ser	Pro	Gly	Ala	Ser	Ser	Arg	Gly	Trp	Asp	Asp	Gly	245	250	255
Asp	Thr	Arg	Ser	Glu	His	Ser	Tyr	Ser	Glu	Ser	Gly	Ala	Ser	Gly	260	265	270
Ser	Ser	Phe	Glu	Glu	Leu	Asp	Leu	Glu	Gly	Glu	Gly	Pro	Leu	Gly	275	280	285
Glu	Ser	Arg	Leu	Asp	Pro	Gly	Thr	Glu	Pro	Leu	Gly	Thr	Thr	Lys	290	295	300
Trp	Leu	Trp	Glu	Pro	Thr	Ala	Pro	Glu	Lys	Gly	Lys	Glu			305	310	

<210> 98

<211> 725

<212> DNA

<213> Homo sapiens

<400> 98

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 cccgctccat ctgctgctgc tgctgctgct cagtgcggcg gtgtgccggg 150  
 ctgaggctgg gctcgaaacc gaaagtcccg tccggaccct ccaagtggag 200  
 accctggtgg agccccaga accatgtgcc gagcccgctg cttttggaga 250

cacgcttcac atacactaca cggaagctt ggtagatgga cgtattattg 300  
 acacctocct gaccagagac cctctgggta tagaacttgg ccaaaagcag 350  
 gtgattccag gtctggagca gagtcttctc gacatgtgtg tgggagagaa 400  
 gogaagggca atcattcctt ctacttggc ctatggaaaa cggggatttc 450  
 caccatctgt cccagcggat gcagtgggtc agtatgacgt ggagctgatt 500  
 gcactaatcc gagccaacta ctggctaaag ctggtgaagg gcattttgcc 550  
 tctggtaggg atggccatgg tgccagccct cctgggcctc attgggtatc 600  
 acctatacag aaaggccaat agacccaaag tctccaaaaa gaagctcaag 650  
 gaagagaaac gaaacaagag caaaaagaaa taataaataa taaattttaa 700  
 aaaacttaaa aaaaaaaaaa aaaaa 725

<210> 99

<211> 201

<212> PRT

<213> Homo sapiens

<400> 99

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Thr	Glu	Ser	Pro	Val	Arg	Thr	Leu	Gln	Val	Glu	Thr	Leu	Val	Glu	35	40	45	
Pro	Pro	Glu	Pro	Cys	Ala	Glu	Pro	Ala	Ala	Phe	Gly	Asp	Thr	Leu	50	55	60	
His	Ile	His	Tyr	Thr	Gly	Ser	Leu	Val	Asp	Gly	Arg	Ile	Ile	Asp	65	70	75	
Thr	Ser	Leu	Thr	Arg	Asp	Pro	Leu	Val	Ile	Glu	Leu	Gly	Gln	Lys	80	85	90	
Gln	Val	Ile	Pro	Gly	Leu	Glu	Gln	Ser	Leu	Leu	Asp	Met	Cys	Val	95	100	105	
Gly	Glu	Lys	Arg	Arg	Ala	Ile	Ile	Pro	Ser	His	Leu	Ala	Tyr	Gly	110	115	120	
Lys	Arg	Gly	Phe	Pro	Pro	Ser	Val	Pro	Ala	Asp	Ala	Val	Val	Gln	125	130	135	
Tyr	Asp	Val	Glu	Leu	Ile	Ala	Leu	Ile	Arg	Ala	Asn	Tyr	Trp	Leu	140	145	150	
Lys	Leu	Val	Lys	Gly	Ile	Leu	Pro	Leu	Val	Gly	Met	Ala	Met	Val	155	160	165	
Pro	Ala	Leu	Leu	Gly	Leu	Ile	Gly	Tyr	His	Leu	Tyr	Arg	Lys	Ala	170	175	180	
Asn	Arg	Pro	Lys	Val	Ser	Lys	Lys	Lys	Leu	Lys	Glu	Glu	Lys	Arg				

Asn Lys Ser Lys Lys Lys  
200

<210> 100  
<211> 705  
<212> DNA  
<213> Homo sapiens

<400> 100  
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cgctccatct gctgctgctg ctgctgctca gtgcggcggt gtgccgggct 150  
gaggctgggc tcgaaaccga aagtcccgctc cggaccctcc aagtggagac 200  
cctggtggag cccccagaac catgtgccga gcccgtgct tttggagaca 250  
cgcttcacat aactacacg ggaagcttgg tagatggacg tattattgac 300  
acctccctga ccagagaccc tctggttata gaacttggcc aaaagcaggt 350  
gattccaggt ctggagcaga gtcttctcga catgtgtgtg ggagagaagc 400  
gaagggcaat cattccttct cacttggcct atggaaaacg gggatttcca 450  
ccatctgtcc cagcggatgc agtgggtgcag tatgacgtgg agctgattgc 500  
actaatccga gccaaactact ggctaaaagct ggtgaagggc attttgcctc 550  
tggtagggat ggccatggtg ccaccctcct gggcctcatt gggtatcacc 600  
tatacagaaa ggccaataga cccaaagtct ccaaaaagaa gctcaaggaa 650  
gagaaacgaa acaagagcaa aaagaaataa taaataataa attttaaaaa 700  
actta 705

<210> 101  
<211> 543  
<212> DNA  
<213> Homo sapiens

<400> 101  
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gaaccatgtg ccgagcccg cgtttttgga gacacgcttc acatacacta 100  
cacgggaagc ttggtagatg gacgtattat tgacacctcc ctgaccagag 150  
accctctggt tatagaactt ggccaaaagc aggtgattcc aggtctggag 200  
cagagtcttc tcgacatgtg tgtgggagag aagcgaaggg caatcattcc 250  
ttctcacttg gcctatggaa aacggggatt tccaccatct gtcccagcgg 300  
atgcagtggg gcagtatgac gtggagctga ttgcactaat ccgagccaac 350  
tactggctaa agctggtgaa gggcattttg cctctggtag ggatggccat 400

ggtgccagcc ctcttgggcc tcattgggta tcacctatac agaaaggcca 450  
atagacccaa agtctccaaa aagaagctca aggaagagaa acgaaaCaag 500  
agcaaaaaga aataataaat aataaatttt aaaaaactta aaa 543

<210> 102  
<211> 1316  
<212> DNA  
<213> Homo sapiens

<400> 102  
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aaatcggggg agtgaggcgg gccggcgcg cgcgacaccg ggctccggaa 100  
ccactgcacg acggggctgg actgacctga aaaaaatgtc tggattttcta 150  
gagggcttga gatgctcaga atgcattgac tggggggaaa agcgcaatac 200  
tattgcttcc attgctgctg gtgtactatt ttttacaggc tgggtggatta 250  
tcatagatgc agctgttatt tatcccacca tgaaagattt caaccactca 300  
taccatgcct gtgggtgttat agcaaccata gccttctctaa tgattaatgc 350  
agtatcgaat ggacaagtcc gaggtgatag ttacagtga ggttgtctgg 400  
gtcaaacagg tgctcgcatt tggcttttctg ttggtttcat gttggccttt 450  
ggatctctga ttgcatctat gtggattctt tttggagggt atgttgctaa 500  
agaaaaagac atagtatacc ctggaattgc tgtatttttc cagaatgcct 550  
tcactttttt tggagggctg gtttttaagt ttggcgcgac tgaagactta 600  
tggcagtga caccatctgat ttcccacagc acaacagccc tgcattgggt 650  
tgttttgttt tttactgctc actcccaccc ttttgtaatg ccattttcta 700  
aacttatttc tgagtgtagt ctcagcttaa agttgtgtaa tactaaaatc 750  
acgagaacac ctaaacaaca accaaaaatc tattgtggta tgcacttgat 800  
taacttataa aatgttagag gaaactttca catgaataat ttttgtcaaa 850  
ttttatcatg gtataatttg taaaaataaa aagaaattac aaaagaaatt 900  
atggatttgt caatgtaagt atttgtcata totgagggtc aaaaccacaa 950  
tgaaagtgct ctgaagattt aatgtgttta ttcaaattgt gtctcttctg 1000  
tgtcaaatgt taaatgaaat ataaacattt tttagttttt aaaatattcc 1050  
gtggtcacaa ttcttcctca ctataattgg tatttacttt taccacaaat 1100  
tctgtgaaca tgtaatgtaa ctggcttttg agggctctcc aaggggtgag 1150  
tggacgtgtt ggaagagaga agcaccatgg tccagccacc aggtccctg 1200  
tgtcccttcc atgggaaggt cttccgctgt gcctctcatt ccaagggcag 1250  
gaagatgtga ctcagccatg acacgtgggt ctgggtgggat gcacagtcac 1300

tccacatcca ccactg 1316

<210> 103

<211> 157

<212> PRT

<213> Homo sapiens

<400> 103

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Trp	Gly	Glu	Lys	Arg	Asn	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Gly	Val
				20					25					30
Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Ile	Ile	Asp	Ala	Ala	Val	Ile
				35					40					45
Tyr	Pro	Thr	Met	Lys	Asp	Phe	Asn	His	Ser	Tyr	His	Ala	Cys	Gly
				50					55					60
Val	Ile	Ala	Thr	Ile	Ala	Phe	Leu	Met	Ile	Asn	Ala	Val	Ser	Asn
				65					70					75
Gly	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Ser	Glu	Gly	Cys	Leu	Gly	Gln
				80					85					90
Thr	Gly	Ala	Arg	Ile	Trp	Leu	Phe	Val	Gly	Phe	Met	Leu	Ala	Phe
				95					100					105
Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Gly	Tyr	Val
				110					115					120
Ala	Lys	Glu	Lys	Asp	Ile	Val	Tyr	Pro	Gly	Ile	Ala	Val	Phe	Phe
				125					130					135
Gln	Asn	Ala	Phe	Ile	Phe	Phe	Gly	Gly	Leu	Val	Phe	Lys	Phe	Gly
				140					145					150
Arg	Thr	Glu	Asp	Leu	Trp	Gln								
				155										

<210> 104

<211> 545

<212> DNA

<213> Homo sapiens

<400> 104

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tggattttcta gagggcttga gatgctcaga atgcattgac tggggggaaa 150  
agcgcaatac tattgcttcc attgctgctg gtgtactatt ttttacaggc 200  
tggttgatta tcatagatgc agctgttatt tatccacca tgaaagattt 250  
caaccactca taccatgcct gtgggtgttat agcaaccata gccttcttaa 300  
tgattaatgc agtatcgaat ggacaagtcc gaggtgatag ttacagtga 350  
ggttgtctgg gtcaaacagg tgctcgcatt tggcttttcg ttggtttcat 400

gttggccttt ggatctctga ttgcatctat gtggattott tttggagggt 450  
atgttgctaa agaaaaagac atagtatacc ctggaattgc tgtatttttc 500  
cagaatgcct tcatcttttt tggagggctg gtttttaagt ttggc 545

<210> 105  
<211> 490  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 31, 39, 108, 145, 179, 219, 412, 479  
<223> unknown base

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agaatgcatg actgggggaa aagcgcaaact actattgctt ccattgctgc 100  
tgggtgtanta ttttttacag gctgggtgat tatcatagat gcagntgtta 150  
tttatccac catgaaagat ttcaaccant cataccatgc ctgtggtgtt 200  
atagcaacca tagccttcnt aatgattaat gcagtatcga atggacaagt 250  
ccgaggtgat agttacagtg aagggtgttt gggtaaaca ggtgctcgca 300  
tttggccttt cgttgggttc atgttggcct ttggatctct gattgcatct 350  
atgtggattc tttttggagg ttatgttgct aaagaaaaag acatagtata 400  
ccctggaatt gntgtatttt tccagaatgc cttcatcttt tttggagggc 450  
tggtttttaa gtttggccgc actgaagant tatggcagtg 490

<210> 106  
<211> 466  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 26, 38, 81, 115, 207, 329, 380, 446, 449  
<223> unknown base

<400> 106  
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aatgtttgga ttttttagagg gcttgagatg ntcagaatgc attgactggg 100  
ggaaaagcgc aatantattg ctttccattg ctgctggtgt actatttttt 150  
acaggggtgg ggattatcat agatgcagct gttatttato ccaccatgaa 200  
agatttnaac cactcatacc atgcctgtgg tgttatagca accatagcct 250  
tcctaattgat taatgcagta tcgaatggac aagtccgagg tgatagttac 300  
agtgaagggt gtttgggtca aacaggtgnt cgcatttggc ttttcgttgg 350  
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ggaggttatg ttgctaaaga aaaagacata gtataccctg gaatttctnt 450  
atccccccag aatgcc 466

<210> 107  
<211> 377  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 52, 67, 70, 78, 105, 144, 150, 209, 266, 268, 282, 310, 331, 356  
<223> unknown base

<400> 107  
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antattgctt ccattgntgn tgggtgnta tttttttaca ggctggtgga 100  
ttatnataga tgcagctgtt atttatccca ccatgaaaga tttnaaccan 150  
tcataccatg cctgtggtgt tatagcaacc atagccttcc taatgattaa 200  
tgcagtatng aatggacaag tccgaggtga tagttacagt gaagggtgtt 250  
tgggtcaaac aggtgntngc atttggcttt tngttggttt catgttggcc 300  
tttgatctn tgattgcatt tatgtggatt ntttttggag gttatgttgc 350  
taaagnaaaa gacatagtat accctgt 377

<210> 108  
<211> 552  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 12, 25, 65, 130, 437, 537  
<223> unknown base

<400> 108  
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ggactgacct gaaaaaatg tttggatttn tagagggtt gagatgctca 150  
gaatgcattg actgggggga aaagcgcaat actattgctt ccattgctgc 200  
tgggtgtacta ttttttacag gctggtggat tatcatagat gcagctgtta 250  
tttatccac catgaaagat ttcaaccact cataccatgc ctgtggtgtt 300  
atagcaacca tagccttcct aatgattaat gcagtatcga atggacaagt 350  
ccgaggtgat agttacagtg aagggtgtct gggtaaaca ggtgctcgca 400  
tttggtttt cgttgggttc atgttggcct ttggatntct gattgcatct 450  
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tg 552

<210> 109  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 109  
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<210> 110  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 110  
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<210> 111  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 111  
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<210> 112  
<211> 3004  
<212> DNA  
<213> Homo sapiens

<400> 112  
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ccgaatcctt tctccgaaga tgtcaaacgg ccccagcgc ccctggtaac 150  
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<210> 113  
 <211> 610  
 <212> PRT  
 <213> Homo sapiens

<400> 113  
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 20 25 30  
 Asn Pro Phe Ser Glu Asp Val Lys Arg Pro Pro Ala Pro Leu Val  
 35 40 45  
 Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser  
 50 55 60  
 Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser  
 65 70 75  
 Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly  
 80 85 90  
 Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys  
 95 100 105

Cys	His	Thr	Phe	Gly	Lys	Asn	Gly	Leu	Glu	Phe	Asp	Thr	Gly	Ile	110	115	120
His	Tyr	Ile	Gly	Arg	Met	Glu	Glu	Gly	Ser	Ile	Gly	Arg	Phe	Ile	125	130	135
Leu	Asp	Gln	Ile	Thr	Glu	Gly	Gln	Leu	Asp	Trp	Ala	Pro	Leu	Ser	140	145	150
Ser	Pro	Phe	Asp	Ile	Met	Val	Leu	Glu	Gly	Pro	Asn	Gly	Arg	Lys	155	160	165
Glu	Tyr	Pro	Met	Tyr	Ser	Gly	Glu	Lys	Ala	Tyr	Ile	Gln	Gly	Leu	170	175	180
Lys	Glu	Lys	Phe	Pro	Gln	Glu	Glu	Ala	Ile	Ile	Asp	Lys	Tyr	Ile	185	190	195
Lys	Leu	Val	Lys	Val	Val	Ser	Ser	Gly	Ala	Pro	His	Ala	Ile	Leu	200	205	210
Leu	Lys	Phe	Leu	Pro	Leu	Pro	Val	Val	Gln	Leu	Leu	Asp	Arg	Cys	215	220	225
Gly	Leu	Leu	Thr	Arg	Phe	Ser	Pro	Phe	Leu	Gln	Ala	Ser	Thr	Gln	230	235	240
Ser	Leu	Ala	Glu	Val	Leu	Gln	Gln	Leu	Gly	Ala	Ser	Ser	Glu	Leu	245	250	255
Gln	Ala	Val	Leu	Ser	Tyr	Ile	Phe	Pro	Thr	Tyr	Gly	Val	Thr	Pro	260	265	270
Asn	His	Ser	Ala	Phe	Ser	Met	His	Ala	Leu	Leu	Val	Asn	His	Tyr	275	280	285
Met	Lys	Gly	Gly	Phe	Tyr	Pro	Arg	Gly	Gly	Ser	Ser	Glu	Ile	Ala	290	295	300
Phe	His	Thr	Ile	Pro	Val	Ile	Gln	Arg	Ala	Gly	Gly	Ala	Val	Leu	305	310	315
Thr	Lys	Ala	Thr	Val	Gln	Ser	Val	Leu	Leu	Asp	Ser	Ala	Gly	Lys	320	325	330
Ala	Cys	Gly	Val	Ser	Val	Lys	Lys	Gly	His	Glu	Leu	Val	Asn	Ile	335	340	345
Tyr	Cys	Pro	Ile	Val	Val	Ser	Asn	Ala	Gly	Leu	Phe	Asn	Thr	Tyr	350	355	360
Glu	His	Leu	Leu	Pro	Gly	Asn	Ala	Arg	Cys	Leu	Pro	Gly	Val	Lys	365	370	375
Gln	Gln	Leu	Gly	Thr	Val	Arg	Pro	Gly	Leu	Gly	Met	Thr	Ser	Val	380	385	390
Phe	Ile	Cys	Leu	Arg	Gly	Thr	Lys	Glu	Asp	Leu	His	Leu	Pro	Ser	395	400	405
Thr	Asn	Tyr	Tyr	Val	Tyr	Tyr	Asp	Thr	Asp	Met	Asp	Gln	Ala	Met	410	415	420

Glu Arg Tyr Val	Ser Met Pro Arg Glu	Glu Ala Ala Glu His Ile	425	430	435
Pro Leu Leu Phe	Phe Ala Phe Pro Ser	Ala Lys Asp Pro Thr Trp	440	445	450
Glu Asp Arg Phe	Pro Gly Arg Ser Thr	Met Ile Met Leu Ile Pro	455	460	465
Thr Ala Tyr Glu	Trp Phe Glu Glu Trp	Gln Ala Glu Leu Lys Gly	470	475	480
Lys Arg Gly Ser	Asp Tyr Glu Thr Phe	Lys Asn Ser Phe Val Glu	485	490	495
Ala Ser Met Ser	Val Val Leu Lys Leu	Phe Pro Gln Leu Glu Gly	500	505	510
Lys Val Glu Ser	Val Thr Ala Gly Ser	Pro Leu Thr Asn Gln Phe	515	520	525
Tyr Leu Ala Ala	Pro Arg Gly Ala Cys	Tyr Gly Ala Asp His Asp	530	535	540
Leu Gly Arg Leu	His Pro Cys Val Met	Ala Ser Leu Arg Ala Gln	545	550	555
Ser Pro Ile Pro	Asn Leu Tyr Leu Thr	Gly Gln Asp Ile Phe Thr	560	565	570
Cys Gly Leu Val	Gly Ala Leu Gln Gly	Ala Leu Leu Cys Ser Ser	575	580	585
Ala Ile Leu Lys	Arg Asn Leu Tyr Ser	Asp Leu Lys Asn Leu Asp	590	595	600
Ser Arg Ile Arg	Ala Gln Lys Lys Lys	Asn	605	610	

<210> 114  
 <211> 1701  
 <212> DNA  
 <213> Homo sapiens

<400> 114  
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 cgtcctcggg tgaagaaggc agccaggatg aatccttaga ttccaagact 200  
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 agttgctggt caaatatttc ttgattcaga agaattctgaa ttagaatcct 300  
 ctattcaaga agaggaagac agcctcaaga gccaagaggg ggaaagtgtc 350  
 acagaagata tcagctttct agagtctcca aatccagaaa acaaggacta 400  
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 tatgatgaat gtacatcaga tgggagggaa gatggcagac tgtggtgtgc 550  
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 aattgttaaa attcatggag ttatttgtgc agaagactc cagagagctc 1450  
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<210> 115  
 <211> 301  
 <212> PRT  
 <213> Homo sapiens

<400> 115  
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				35					40					45
Lys	Asp	His	Thr	Thr	Ala	Gly	Arg	Val	Val	Ala	Gly	Gln	Ile	Phe
				50					55					60
Leu	Asp	Ser	Glu	Glu	Ser	Glu	Leu	Glu	Ser	Ser	Ile	Gln	Glu	Glu
				65					70					75
Glu	Asp	Ser	Leu	Lys	Ser	Gln	Glu	Gly	Glu	Ser	Val	Thr	Glu	Asp
				80					85					90
Ile	Ser	Phe	Leu	Glu	Ser	Pro	Asn	Pro	Glu	Asn	Lys	Asp	Tyr	Glu
				95					100					105
Glu	Pro	Lys	Lys	Val	Arg	Lys	Pro	Ala	Leu	Thr	Ala	Ile	Glu	Gly
				110					115					120
Thr	Ala	His	Gly	Glu	Pro	Cys	His	Phe	Pro	Phe	Leu	Phe	Leu	Asp
				125					130					135
Lys	Glu	Tyr	Asp	Glu	Cys	Thr	Ser	Asp	Gly	Arg	Glu	Asp	Gly	Arg
				140					145					150
Leu	Trp	Cys	Ala	Thr	Thr	Tyr	Asp	Tyr	Lys	Ala	Asp	Glu	Lys	Trp
				155					160					165
Gly	Phe	Cys	Glu	Thr	Glu	Glu	Glu	Ala	Ala	Lys	Arg	Arg	Gln	Met
				170					175					180
Gln	Glu	Ala	Glu	Met	Met	Tyr	Gln	Thr	Gly	Met	Lys	Ile	Leu	Asn
				185					190					195
Gly	Ser	Asn	Lys	Lys	Ser	Gln	Lys	Arg	Glu	Ala	Tyr	Arg	Tyr	Leu
				200					205					210
Gln	Lys	Ala	Ala	Ser	Met	Asn	His	Thr	Lys	Ala	Leu	Glu	Arg	Val
				215					220					225
Ser	Tyr	Ala	Leu	Leu	Phe	Gly	Asp	Tyr	Leu	Pro	Gln	Asn	Ile	Gln
				230					235					240
Ala	Ala	Arg	Glu	Met	Phe	Glu	Lys	Leu	Thr	Glu	Glu	Gly	Ser	Pro
				245					250					255
Lys	Gly	Gln	Thr	Ala	Leu	Gly	Phe	Leu	Tyr	Ala	Ser	Gly	Leu	Gly
				260					265					270
Val	Asn	Ser	Ser	Gln	Ala	Lys	Ala	Leu	Val	Tyr	Tyr	Thr	Phe	Gly
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Ala	Leu	Gly	Gly	Asn	Leu	Ile	Ala	His	Met	Val	Leu	Val	Ser	Arg
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Leu

<210> 116  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens  
 <400> 116

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 aaaatgggtt aataatattc aacatgtcaa caac 584

<210> 117  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 117  
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 Phe Pro Gly Gln Val Ala Gln Leu Ser Cys Thr Leu Ser Pro Gln  
 35 40 45  
 His Val Thr Ile Arg Asp Tyr Gly Val Ser Trp Tyr Gln Gln Arg  
 50 55 60  
 Ala Gly Ser Ala Pro Arg Tyr Leu Leu Tyr Tyr Arg Ser Glu Glu  
 65 70 75  
 Asp His His Arg Pro Ala Asp Ile Pro Asp Arg Phe Ser Ala Ala  
 80 85 90  
 Lys Asp Glu Ala His Asn Ala Cys Val Leu Thr Ile Ser Pro Val  
 95 100 105  
 Gln Pro Glu Asp Asp Ala Asp Tyr Tyr Cys Ser Val Gly Tyr Gly  
 110 115 120  
 Phe Ser Pro

<210> 118  
 <211> 3402  
 <212> DNA  
 <213> Homo sapiens  
 <400> 118

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 aa 3402

<210> 119  
 <211> 504  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Thr Val Arg Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu  
 50 55 60  
 Thr Met Trp Thr Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser  
 65 70 75  
 Arg Phe Arg Val Leu Pro Gln Gly Leu Lys Val Lys Gln Val Glu  
 80 85 90  
 Arg Glu Asp Ala Gly Val Tyr Val Cys Lys Ala Thr Asn Gly Phe  
 95 100 105  
 Gly Ser Leu Ser Val Asn Tyr Thr Leu Val Val Leu Asp Asp Ile  
 110 115 120  
 Ser Pro Gly Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly  
 125 130 135  
 Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr  
 140 145 150  
 Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly  
 155 160 165  
 Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro  
 170 175 180  
 Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu  
 185 190 195  
 Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn  
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 Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn  
 215 220 225  
 Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln  
 230 235 240

Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
				245					250					255
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
				260					265					270
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu
				275					280					285
Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly
				290					295					300
Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro
				305					310					315
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
				320					325					330
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly
				335					340					345
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys
				350					355					360
Pro	Pro	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu
				365					370					375
Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile
				380					385					390
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro
				395					400					405
Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro
				410					415					420
Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu
				425					430					435
Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His
				440					445					450
Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val
				455					460					465
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr
				470					475					480
His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys
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Val	His	Gln	His	Ile	His	Tyr	Gln	Cys						
				500										

<210> 120

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

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<210> 121

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

cggttcgaca cgcggcaggt g 21

<210> 122

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

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<210> 123

<211> 4420

<212> DNA

<213> Homo sapiens

<400> 123

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gcctgggtgt tctccttcct ggtcctggaa gtcacatctg tgttggggag 200

acagacgatg ctacccagt cagtaagaag agtccagcct gggaagaaga 250

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<210> 124

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Gly	Thr	Lys	Ala	Trp	Val	Phe	Ser	Phe	Leu	Val	Leu	Glu	1	5	10	15
Val	Thr	Ser	Val	Leu	Gly	Arg	Gln	Thr	Met	Leu	Thr	Gln	Ser	Val	20	25	30	
Arg	Arg	Val	Gln	Pro	Gly	Lys	Lys	Asn	Pro	Ser	Ile	Phe	Ala	Lys	35	40	45	
Pro	Ala	Asp	Thr	Leu	Glu	Ser	Pro	Gly	Glu	Trp	Thr	Thr	Trp	Phe	50	55	60	
Asn	Ile	Asp	Tyr	Pro	Gly	Gly	Lys	Gly	Asp	Tyr	Glu	Arg	Leu	Asp	65	70	75	
Ala	Ile	Arg	Phe	Tyr	Tyr	Gly	Asp	Arg	Val	Cys	Ala	Arg	Pro	Leu	80	85	90	
Arg	Leu	Glu	Ala	Arg	Thr	Thr	Asp	Trp	Thr	Pro	Ala	Gly	Ser	Thr	95	100	105	
Gly	Gln	Val	Val	His	Gly	Ser	Pro	Arg	Glu	Gly	Phe	Trp	Cys	Leu	110	115	120	
Asn	Arg	Glu	Gln	Arg	Pro	Gly	Gln	Asn	Cys	Ser	Asn	Tyr	Thr	Val	125	130	135	
Arg	Phe	Leu	Cys	Pro	Pro	Gly	Ser	Leu	Arg	Arg	Asp	Thr	Glu	Arg	140	145	150	
Ile	Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Lys	Cys	Ser	Ala	Ala	Cys	155	160	165	
Gly	Gln	Thr	Gly	Val	Gln	Thr	Arg	Thr	Arg	Ile	Cys	Leu	Ala	Glu	170	175	180	
Met	Val	Ser	Leu	Cys	Ser	Glu	Ala	Ser	Glu	Glu	Gly	Gln	His	Cys	185	190	195	
Met	Gly	Gln	Asp	Cys	Thr	Ala	Cys	Asp	Leu	Thr	Cys	Pro	Met	Gly	200	205	210	

Gln	Val	Asn	Ala	Asp	Cys	Asp	Ala	Cys	Met	Cys	Gln	Asp	Phe	Met	215	220	225
Leu	His	Gly	Ala	Val	Ser	Leu	Pro	Gly	Gly	Ala	Pro	Ala	Ser	Gly	230	235	240
Ala	Ala	Ile	Tyr	Leu	Leu	Thr	Lys	Thr	Pro	Lys	Leu	Leu	Thr	Gln	245	250	255
Thr	Asp	Ser	Asp	Gly	Arg	Phe	Arg	Ile	Pro	Gly	Leu	Cys	Pro	Asp	260	265	270
Gly	Lys	Ser	Ile	Leu	Lys	Ile	Thr	Lys	Val	Lys	Phe	Ala	Pro	Ile	275	280	285
Val	Leu	Thr	Met	Pro	Lys	Thr	Ser	Leu	Lys	Ala	Ala	Thr	Ile	Lys	290	295	300
Ala	Glu	Phe	Val	Arg	Ala	Glu	Thr	Pro	Tyr	Met	Val	Met	Asn	Pro	305	310	315
Glu	Thr	Lys	Ala	Arg	Arg	Ala	Gly	Gln	Ser	Val	Ser	Leu	Cys	Cys	320	325	330
Lys	Ala	Thr	Gly	Lys	Pro	Arg	Pro	Asp	Lys	Tyr	Phe	Trp	Tyr	His	335	340	345
Asn	Asp	Thr	Leu	Leu	Asp	Pro	Ser	Leu	Tyr	Lys	His	Glu	Ser	Lys	350	355	360
Leu	Val	Leu	Arg	Lys	Leu	Gln	Gln	His	Gln	Ala	Gly	Glu	Tyr	Phe	365	370	375
Cys	Lys	Ala	Gln	Ser	Asp	Ala	Gly	Ala	Val	Lys	Ser	Lys	Val	Ala	380	385	390
Gln	Leu	Ile	Val	Thr	Ala	Ser	Asp	Glu	Thr	Pro	Cys	Asn	Pro	Val	395	400	405
Pro	Glu	Ser	Tyr	Leu	Ile	Arg	Leu	Pro	His	Asp	Cys	Phe	Gln	Asn	410	415	420
Ala	Thr	Asn	Ser	Phe	Tyr	Tyr	Asp	Val	Gly	Arg	Cys	Pro	Val	Lys	425	430	435
Thr	Cys	Ala	Gly	Gln	Gln	Asp	Asn	Gly	Ile	Arg	Cys	Arg	Asp	Ala	440	445	450
Val	Gln	Asn	Cys	Cys	Gly	Ile	Ser	Lys	Thr	Glu	Glu	Arg	Glu	Ile	455	460	465
Gln	Cys	Ser	Gly	Tyr	Thr	Leu	Pro	Thr	Lys	Val	Ala	Lys	Glu	Cys	470	475	480
Ser	Cys	Gln	Arg	Cys	Thr	Glu	Thr	Arg	Ser	Ile	Val	Arg	Gly	Arg	485	490	495
Val	Ser	Ala	Ala	Asp	Asn	Gly	Glu	Pro	Met	Arg	Phe	Gly	His	Val	500	505	510
Tyr	Met	Gly	Asn	Ser	Arg	Val	Ser	Met	Thr	Gly	Tyr	Lys	Gly	Thr	515	520	525

Phe Thr Leu His	Val	Pro Gln Asp Thr	Glu	Arg Leu Val Leu Thr	530	535	540
Phe Val Asp Arg	Leu Gln Lys Phe Val	Asn Thr Thr Lys Val Leu	545	550	555		
Pro Phe Asn Lys	Lys Gly Ser Ala Val	Phe His Glu Ile Lys Met	560	565	570		
Leu Arg Arg Lys	Glu Pro Ile Thr Leu	Glu Ala Met Glu Thr Asn	575	580	585		
Ile Ile Pro Leu	Gly Glu Val Val Gly	Glu Asp Pro Met Ala Glu	590	595	600		
Leu Glu Ile Pro	Ser Arg Ser Phe Tyr	Arg Gln Asn Gly Glu Pro	605	610	615		
Tyr Ile Gly Lys	Val Lys Ala Ser Val	Thr Phe Leu Asp Pro Arg	620	625	630		
Asn Ile Ser Thr	Ala Thr Ala Ala Gln	Thr Asp Leu Asn Phe Ile	635	640	645		
Asn Asp Glu Gly	Asp Thr Phe Pro Leu	Arg Thr Tyr Gly Met Phe	650	655	660		
Ser Val Asp Phe	Arg Asp Glu Val Thr	Ser Glu Pro Leu Asn Ala	665	670	675		
Gly Lys Val Lys	Val His Leu Asp Ser	Thr Gln Val Lys Met Pro	680	685	690		
Glu His Ile Ser	Thr Val Lys Leu Trp	Ser Leu Asn Pro Asp Thr	695	700	705		
Gly Leu Trp Glu	Glu Glu Gly Asp Phe	Lys Phe Glu Asn Gln Arg	710	715	720		
Arg Asn Lys Arg	Glu Asp Arg Thr Phe	Leu Val Gly Asn Leu Glu	725	730	735		
Ile Arg Glu Arg	Arg Leu Phe Asn Leu	Asp Val Pro Glu Ser Arg	740	745	750		
Arg Cys Phe Val	Lys Val Arg Ala Tyr	Arg Ser Glu Arg Phe Leu	755	760	765		
Pro Ser Glu Gln	Ile Gln Gly Val Val	Ile Ser Val Ile Asn Leu	770	775	780		
Glu Pro Arg Thr	Gly Phe Leu Ser Asn	Pro Arg Ala Trp Gly Arg	785	790	795		
Phe Asp Ser Val	Ile Thr Gly Pro Asn	Gly Ala Cys Val Pro Ala	800	805	810		
Phe Cys Asp Asp	Gln Ser Pro Asp Ala	Tyr Ser Ala Tyr Val Leu	815	820	825		
Ala Ser Leu Ala	Gly Glu Glu Leu Gln	Ala Val Glu Ser Ser Pro	830	835	840		

Lys	Phe	Asn	Pro	Asn	Ala	Ile	Gly	Val	Pro	Gln	Pro	Tyr	Leu	Asn	
				845					850					855	
Lys	Leu	Asn	Tyr	Arg	Arg	Thr	Asp	His	Glu	Asp	Pro	Arg	Val	Lys	
				860					865					870	
Lys	Thr	Ala	Phe	Gln	Ile	Ser	Met	Ala	Lys	Pro	Arg	Pro	Asn	Ser	
				875					880					885	
Ala	Glu	Glu	Ser	Asn	Gly	Pro	Ile	Tyr	Ala	Phe	Glu	Asn	Leu	Arg	
				890					895					900	
Ala	Cys	Glu	Glu	Ala	Pro	Pro	Ser	Ala	Ala	His	Phe	Arg	Phe	Tyr	
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Gln	Ile	Glu	Gly	Asp	Arg	Tyr	Asp	Tyr	Asn	Thr	Val	Pro	Phe	Asn	
				920					925					930	
Glu	Asp	Asp	Pro	Met	Ser	Trp	Thr	Glu	Asp	Tyr	Leu	Ala	Trp	Trp	
				935					940					945	
Pro	Lys	Pro	Met	Glu	Phe	Arg	Ala	Cys	Tyr	Ile	Lys	Val	Lys	Ile	
				950					955					960	
Val	Gly	Pro	Leu	Glu	Val	Asn	Val	Arg	Ser	Arg	Asn	Met	Gly	Gly	
				965					970					975	
Thr	His	Arg	Arg	Thr	Val	Gly	Lys	Leu	Tyr	Gly	Ile	Arg	Asp	Val	
				980					985					990	
Arg	Ser	Thr	Arg	Asp	Arg	Asp	Gln	Pro	Asn	Val	Ser	Ala	Ala	Cys	
				995					1000					1005	
Leu	Glu	Phe	Lys	Cys	Ser	Gly	Met	Leu	Tyr	Asp	Gln	Asp	Arg	Val	
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Asp	Arg	Thr	Leu	Val	Lys	Val	Ile	Pro	Gln	Gly	Ser	Cys	Arg	Arg	
				1025					1030					1035	
Ala	Ser	Val	Asn	Pro	Met	Leu	His	Glu	Tyr	Leu	Val	Asn	His	Leu	
				1040					1045					1050	
Pro	Leu	Ala	Val	Asn	Asn	Asp	Thr	Ser	Glu	Tyr	Thr	Met	Leu	Ala	
				1055					1060					1065	
Pro	Leu	Asp	Pro	Leu	Gly	His	Asn	Tyr	Gly	Ile	Tyr	Thr	Val	Thr	
				1070					1075					1080	
Asp	Gln	Asp	Pro	Arg	Thr	Ala	Lys	Glu	Ile	Ala	Leu	Gly	Arg	Cys	
				1085					1090					1095	
Phe	Asp	Gly	Thr	Ser	Asp	Gly	Ser	Ser	Arg	Ile	Met	Lys	Ser	Asn	
				1100					1105					1110	
Val	Gly	Val	Ala	Leu	Thr	Phe	Asn	Cys	Val	Glu	Arg	Gln	Val	Gly	
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Arg	Gln	Ser	Ala	Phe	Gln	Tyr	Leu	Gln	Ser	Thr	Pro	Ala	Gln	Ser	
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Pro	Ala	Ala	Gly	Thr	Val	Gln	Gly	Arg	Val	Pro	Ser	Arg	Arg	Gln	
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Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Gly Gly Val Val Ala  
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Ser Leu Arg Phe Pro Arg Val Ala Gln Gln Pro Leu Ile Asn  
 1175 1180

<210> 125  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 125  
 ctggtgcctc aacagggagc ag 22

<210> 126  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 126  
 ccattgtgca ggtcaggtca cag 23

<210> 127  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 127  
 ctggagcaag tgctcagctg cctgtggtca gactggggtc 40

<210> 128  
 <211> 2819  
 <212> DNA  
 <213> Homo sapiens

<400> 128  
 ctgcaagttg ttaacgccta acacacaagt atgttaggct tccaccaaag 50  
 tcctcaatat acctgaatac gcacaatatc ttaactcttc atatttggtt 100  
 ttgggatctg ctttgaggtc ccatcttcat ttaaaaaaaaa atacagagac 150  
 ctacctaccc gtacgcatac atacatatgt gtatatatat gtaaaactaga 200  
 caaagatcgc agatcataaa gcaagctctg ctttagtttc caagaagatt 250  
 acaaagaatt tagagatgta ttgtcaaga tccctgtcga ttcatgccct 300  
 ttgggttacg gtgtcctcag tgatgcagcc ctaccctttg gtttggggac 350  
 attatgattt gtgtaagact cagatttaca cggaagaagg gaaagtttgg 400  
 gattacatgg cctgccagcc ggaatccacg gacatgacaa aatatctgaa 450

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 aggggtataca acaaatagca aaataatcca ctttgaaatc aaagacaggt 950  
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 aacaagtgtg ataagattcc accaaaggac attctaaatg ttttcttggt 2550  
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 caggaatttg tattgcaatt tcttaagatg aaaggaacag ccaccaagca 2650  
 gtttcacact cactttactg atttctgtgt ggactgagta cattcagctg 2700  
 acgaatttag ttcccaggaa gatggattga tgttcactag cttggacaac 2750  
 ttctgcaaaa tatgagacta ttccacttg ggaaaaatta caacagcaaa 2800  
 aaaaaaaaaa aaaaaaaaaa 2819

<210> 129  
 <211> 438  
 <212> PRT  
 <213> Homo sapiens

<400> 129  
 Met Tyr Leu Ser Arg Ser Leu Ser Ile His Ala Leu Trp Val Thr  
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 Val Ser Ser Val Met Gln Pro Tyr Pro Leu Val Trp Gly His Tyr  
 20 25 30  
 Asp Leu Cys Lys Thr Gln Ile Tyr Thr Glu Glu Gly Lys Val Trp  
 35 40 45  
 Asp Tyr Met Ala Cys Gln Pro Glu Ser Thr Asp Met Thr Lys Tyr  
 50 55 60  
 Leu Lys Val Lys Leu Asp Pro Pro Asp Ile Thr Cys Gly Asp Pro  
 65 70 75  
 Pro Glu Thr Phe Cys Ala Met Gly Asn Pro Tyr Met Cys Asn Asn  
 80 85 90  
 Glu Cys Asp Ala Ser Thr Pro Glu Leu Ala His Pro Pro Glu Leu  
 95 100 105  
 Met Phe Asp Phe Glu Gly Arg His Pro Ser Thr Phe Trp Gln Ser  
 110 115 120  
 Ala Thr Trp Lys Glu Tyr Pro Lys Pro Leu Gln Val Asn Ile Thr

	125		130		135
Leu Ser Trp Ser	Lys Thr Ile Glu Leu	Thr Asp Asn Ile Val	Ile		
	140		145		150
Thr Phe Glu Ser	Gly Arg Pro Asp Gln	Met Ile Leu Glu Lys	Ser		
	155		160		165
Leu Asp Tyr Gly	Arg Thr Trp Gln Pro	Tyr Gln Tyr Tyr Ala	Thr		
	170		175		180
Asp Cys Leu Asp	Ala Phe His Met Asp	Pro Lys Ser Val Lys	Asp		
	185		190		195
Leu Ser Gln His	Thr Val Leu Glu Ile	Ile Cys Thr Glu Glu	Tyr		
	200		205		210
Ser Thr Gly Tyr	Thr Thr Asn Ser Lys	Ile Ile His Phe Glu	Ile		
	215		220		225
Lys Asp Arg Phe	Ala Leu Phe Ala Gly	Pro Arg Leu Arg Asn	Met		
	230		235		240
Ala Ser Leu Tyr	Gly Gln Leu Asp Thr	Thr Lys Lys Leu Arg	Asp		
	245		250		255
Phe Phe Thr Val	Thr Asp Leu Arg Ile	Arg Leu Leu Arg Pro	Ala		
	260		265		270
Val Gly Glu Ile	Phe Val Asp Glu Leu	His Leu Ala Arg Tyr	Phe		
	275		280		285
Tyr Ala Ile Ser	Asp Ile Lys Val Arg	Gly Arg Cys Lys Cys	Asn		
	290		295		300
Leu His Ala Thr	Val Cys Val Tyr Asp	Asn Ser Lys Leu Thr	Cys		
	305		310		315
Glu Cys Glu His	Asn Thr Thr Gly Pro	Asp Cys Gly Lys Cys	Lys		
	320		325		330
Lys Asn Tyr Gln	Gly Arg Pro Trp Ser	Pro Gly Ser Tyr Leu	Pro		
	335		340		345
Ile Pro Lys Gly	Thr Ala Asn Thr Cys	Ile Pro Ser Ile Ser	Ser		
	350		355		360
Ile Gly Thr Asn	Val Cys Asp Asn Glu	Leu Leu His Cys Gln	Asn		
	365		370		375
Gly Gly Thr Cys	His Asn Asn Val Arg	Cys Leu Cys Pro Ala	Ala		
	380		385		390
Tyr Thr Gly Ile	Leu Cys Glu Lys Leu	Arg Cys Glu Glu Ala	Gly		
	395		400		405
Ser Cys Gly Ser	Asp Ser Gly Gln Gly	Ala Pro Pro His Gly	Thr		
	410		415		420
Pro Ala Leu Leu	Leu Leu Thr Thr Leu	Leu Gly Thr Ala Ser	Pro		
	425		430		435
Leu Val Phe					

<210> 130  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 130  
tcgattatgg acgaacatgg cagc 24

<210> 131  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 131  
ttctgagatc cctcatcctc 20

<210> 132  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 132  
aggttcaggg acagcaagtt tggg 24

<210> 133  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 133  
tttgctggac ctcggtacg gaattggctt ccctctacgg acagctggat 50

<210> 134  
<211> 1493  
<212> DNA  
<213> Homo sapiens

<400> 134  
cccacgcgtc cgggtgacct gggccgagcc ctcccggtcg gctaagattg 50  
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ccgggcgagg tgtcctcatg acttctcttg tggaccatgt ccgtgatctt 150  
ttttgcctgc gtggtacggg taagggatgg actgcccctc tcagcctcta 200  
ctgattttta ccacacccaa gatttttttg aatggaggag acgggtcaag 250  
agtttagcct tgcgactggc ccagtatcca ggtcgagggt ctgcagaagg 300

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 accctgtggt gggaattcac agcttctctat gacactacct gcattggcct 450  
 agcctccagg ccatacgttt ttcttgagtt tgacagcatc attcagaaaag 500  
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 gaaaaaattc aggaggagct caagttgcag cctccagcgg ttctcactct 600  
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 gcataaaata ctgaggctga tttagtcagg gcaaaacat ttactttaca 1250  
 tattcgtttt caatacttgc tgttcatgtt acacaagctt cttacggttt 1300  
 tcttgtaaca ataaatatat tgagtaaata atgggtacat tttaacaaac 1350  
 tcagtagtac aacctaaact tgtataaaag tgtgtaaaaa tgtatagcca 1400  
 tttatatcct atgtataaat taaatgaggt ggcttcagaa atggcagaat 1450  
 aaatctaaag tgtttattaa aaaaaaaaaa aaaaaaaaaa aag 1493

<210> 135

<211> 228

<212> PRT

<213> Homo sapiens

<400> 135

Met	Ser	Val	Ile	Phe	Phe	Ala	Cys	Val	Val	Arg	Val	Arg	Asp	Gly
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Leu	Pro	Leu	Ser	Ala	Ser	Thr	Asp	Phe	Tyr	His	Thr	Gln	Asp	Phe
				20					25					30

Leu	Glu	Trp	Arg	Arg	Arg	Leu	Lys	Ser	Leu	Ala	Leu	Arg	Leu	Ala
				35					40					45

Gln	Tyr	Pro	Gly	Arg	Gly	Ser	Ala	Glu	Gly	Cys	Asp	Phe	Ser	Ile	50	55	60
His	Phe	Ser	Ser	Phe	Gly	Asp	Val	Ala	Cys	Met	Ala	Ile	Cys	Ser	65	70	75
Cys	Gln	Cys	Pro	Ala	Ala	Met	Ala	Phe	Cys	Phe	Leu	Glu	Thr	Leu	80	85	90
Trp	Trp	Glu	Phe	Thr	Ala	Ser	Tyr	Asp	Thr	Thr	Cys	Ile	Gly	Leu	95	100	105
Ala	Ser	Arg	Pro	Tyr	Ala	Phe	Leu	Glu	Phe	Asp	Ser	Ile	Ile	Gln	110	115	120
Lys	Val	Lys	Trp	His	Phe	Asn	Tyr	Val	Ser	Ser	Ser	Gln	Met	Glu	125	130	135
Cys	Ser	Leu	Glu	Lys	Ile	Gln	Glu	Glu	Leu	Lys	Leu	Gln	Pro	Pro	140	145	150
Ala	Val	Leu	Thr	Leu	Glu	Asp	Thr	Asp	Val	Ala	Asn	Gly	Val	Met	155	160	165
Asn	Gly	His	Thr	Pro	Met	His	Leu	Glu	Pro	Ala	Pro	Asn	Phe	Arg	170	175	180
Met	Glu	Pro	Val	Thr	Ala	Leu	Gly	Ile	Leu	Ser	Leu	Ile	Leu	Asn	185	190	195
Ile	Met	Cys	Ala	Ala	Leu	Asn	Leu	Ile	Arg	Gly	Val	His	Leu	Ala	200	205	210
Glu	His	Ser	Leu	Gln	Asp	Pro	Arg	Ser	Trp	Phe	Cys	Trp	Leu	Asp	215	220	225

Gln Thr Ser

<210> 136  
 <211> 239  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 39, 61, 143, 209  
 <223> unknown base

<400> 136  
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 tcattcagaa agtgaagtgg cattttaact atgtaagttc ctntcagatg 150  
 gagtgcagct tggaaaaaat tcaggaggag ctcaagttgc agcctccagc 200  
 ggttctcant atggaggaca cagatgtggc aaatggggt 239

<210> 137  
 <211> 2300  
 <212> DNA

<213> Homo sapiens

<400> 137

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ccctttaaaa cgaggcgggt ggtgcctgcc cctttaaggg cggggcgtcc 150  
ggacgactgt atctgagccc cagactgccg cgagtttctg tcgcaggctg 200  
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<210> 138  
 <211> 489  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
 Met Glu Ala Pro Asp Tyr Glu Val Leu Ser Val Arg Glu Gln Leu  
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 Phe His Glu Arg Ile Arg Glu Cys Ile Ile Ser Thr Leu Leu Phe  
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 Ala Thr Leu Tyr Ile Leu Cys His Ile Phe Leu Thr Arg Phe Lys  
 35 40 45  
 Lys Pro Ala Glu Phe Thr Thr Val Asp Asp Glu Asp Ala Thr Val  
 50 55 60  
 Asn Lys Ile Ala Leu Glu Leu Cys Thr Phe Thr Leu Ala Ile Ala  
 65 70 75  
 Leu Gly Ala Val Leu Leu Leu Pro Phe Ser Ile Ile Ser Asn Glu  
 80 85 90  
 Val Leu Leu Ser Leu Pro Arg Asn Tyr Tyr Ile Gln Trp Leu Asn  
 95 100 105  
 Gly Ser Leu Ile His Gly Leu Trp Asn Leu Val Phe Leu Phe Pro  
 110 115 120  
 Asn Leu Ser Leu Ile Phe Leu Met Pro Phe Ala Tyr Phe Phe Thr

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Glu	Ser	Glu	Gly	Phe	Ala	Gly	Ser	Arg	Lys	Gly	Val	Leu	Gly	Arg
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Val	Tyr	Glu	Thr	Val	Val	Met	Leu	Met	Leu	Leu	Thr	Leu	Leu	Val
				155					160					165
Leu	Gly	Met	Val	Trp	Val	Ala	Ser	Ala	Ile	Val	Asp	Lys	Asn	Lys
				170					175					180
Ala	Asn	Arg	Glu	Ser	Leu	Tyr	Asp	Phe	Trp	Glu	Tyr	Tyr	Leu	Pro
				185					190					195
Tyr	Leu	Tyr	Ser	Cys	Ile	Ser	Phe	Leu	Gly	Val	Leu	Leu	Leu	Leu
				200					205					210
Val	Cys	Thr	Pro	Leu	Gly	Leu	Ala	Arg	Met	Phe	Ser	Val	Thr	Gly
				215					220					225
Lys	Leu	Leu	Val	Lys	Pro	Arg	Leu	Leu	Glu	Asp	Leu	Glu	Glu	Gln
				230					235					240
Leu	Tyr	Cys	Ser	Ala	Phe	Glu	Glu	Ala	Ala	Leu	Thr	Arg	Arg	Ile
				245					250					255
Cys	Asn	Pro	Thr	Ser	Cys	Trp	Leu	Pro	Leu	Asp	Met	Glu	Leu	Leu
				260					265					270
His	Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	Arg	Val	Leu	Leu	Glu
				275					280					285
Lys	Arg	Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	Leu	Gly	Tyr	Pro
				290					295					300
Leu	Ala	Met	Leu	Cys	Leu	Leu	Val	Leu	Thr	Gly	Leu	Ser	Val	Leu
				305					310					315
Ile	Val	Ala	Ile	His	Ile	Leu	Glu	Leu	Leu	Ile	Asp	Glu	Ala	Ala
				320					325					330
Met	Pro	Arg	Gly	Met	Gln	Gly	Thr	Ser	Leu	Gly	Gln	Val	Ser	Phe
				335					340					345
Ser	Lys	Leu	Gly	Ser	Phe	Gly	Ala	Val	Ile	Gln	Val	Val	Leu	Ile
				350					355					360
Phe	Tyr	Leu	Met	Val	Ser	Ser	Val	Val	Gly	Phe	Tyr	Ser	Ser	Pro
				365					370					375
Leu	Phe	Arg	Ser	Leu	Arg	Pro	Arg	Trp	His	Asp	Thr	Ala	Met	Thr
				380					385					390
Gln	Ile	Ile	Gly	Asn	Cys	Val	Cys	Leu	Leu	Val	Leu	Ser	Ser	Ala
				395					400					405
Leu	Pro	Val	Phe	Ser	Arg	Thr	Leu	Gly	Leu	Thr	Arg	Phe	Asp	Leu
				410					415					420
Leu	Gly	Asp	Phe	Gly	Arg	Phe	Asn	Trp	Leu	Gly	Asn	Phe	Tyr	Ile
				425					430					435
Val	Phe	Leu	Tyr	Asn	Ala	Ala	Phe	Ala	Gly	Leu	Thr	Thr	Leu	Cys

440	445	450
Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu Ile Arg		
455	460	465
Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe Pro		
470	475	480
Gln Ala Ser Arg Lys Thr Gln His Gln		
485		

<210> 139  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 53, 57  
 <223> unknown base

<400> 139  
 ggctgccgag ggaaggcccc ttgggttggt ctggttgct tggcggcggc 50  
 ggnnttcntcc ccgctcgcc tccccggggc cagaggcacc tcggcttcag 100  
 tcatgctgag cagagtatgg aagcacctga ctacgaagtg ctatccgtgc 150  
 gagaacagct attccacgag aggatccgag agtgtattat atcaaacactt 200  
 ctgtttgcaa cactgtacat cctctgccac atcttcctga cccgcttcaa 250  
 gaagcctgct gagttcacca cagtggatga tgaagatgcc accg 294

<210> 140  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 197, 349  
 <223> unknown base

<400> 140  
 gaccgacctt aaagagtggg agcaaaggga ggacagagcc ttttaaaacg 50  
 aggcggtggt gcctgccctt taagggcggg gcgtccggac gactgtatct 100  
 gagccccaga ctgccccgag tttctgtcgc aggctgcgag gaaaggcccc 150  
 taggtggtg ctggtgcttg gggcgggcgg cttcctcccc gttgtcntcc 200  
 ccggggccag aggcacctcg gcttcagtca tgctgagcag agtatggaag 250  
 cacctgacta cgaagtgcta tccgtgcgag aacagctatt ccacgagagg 300  
 atccgcgagt gtattatata aacacttctg tttgcaacac tgtacatcnt 350  
 ctgccacatc ttctgaccc gcttcaagaa gcctgctgag ttcaccacag 400  
 tggatgatga agatgccacc gtcaacaaga ttgcgctcga gctgtgcacc 450

tttacccctgg caattgccct ggggtgctgtc ctgctcctgc ccttctccat 500  
catcagcaat gaggtgctgc actccc 526

<210> 141  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 141  
gactgtatct gagccccaga ctgc 24

<210> 142  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 142  
tcagcaatga ggtgctgctc 20

<210> 143  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 143  
tgaggaagat gagggacagg ttgg 24

<210> 144  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 144  
tatggaagca cctgactacg aagtgcctatc cgtgcgagaa cagctattcc 50

<210> 145  
<211> 685  
<212> DNA  
<213> Homo sapiens

<400> 145  
gatgtgctcc ttggagctgg tgtgcagtgt cctgactgta agatcaagtc 50  
caaacctgtt ttggaattga ggaaacttct cttttgatct cagccottgg 100  
tggtccaggt cttcatgctg ctgtgggtga tattactggg cctggctcct 150  
gtcagtggac agtttgcaag gacaccacag cccattattt tccctcagcc 200  
tccatggacc acagtcttcc aaggagagag agtgaccctc acttgcaagg 250

gatttcgctt ctactcacca cagaaaaaca aatggtacca tcggtacctt 300  
 gggaaagaaa tactaagaga aaccccagac aatatccttg aggttcagga 350  
 atctggagag tacagatgcc agggccaggg ctcccctctc agtagccctg 400  
 tgcacttggg tttttcttca gagatgggat ttcctcatgc tgcccaggct 450  
 aatgttgaac tcttgggctc aagtgatctg ctcacctagg cctctcaaag 500  
 cgctgggatt acagcttcgc tgatcctgca agctccactt tctgtgtttg 550  
 aaggagactc tgtggttctg aggtgccggg caaaggcgga agtaacactg 600  
 aataatacta tttaacaaga tgataatgtc ctggcattcc ttaataaaaag 650  
 aactgacttc caaaaaaaaa aaaaaaaaaa aaaaa 685

<210> 146

<211> 124

<212> PRT

<213> Homo sapiens

<400> 146

Met	Leu	Leu	Trp	Val	Ile	Leu	Leu	Val	Leu	Ala	Pro	Val	Ser	Gly
1				5					10					15
Gln	Phe	Ala	Arg	Thr	Pro	Arg	Pro	Ile	Ile	Phe	Leu	Gln	Pro	Pro
				20					25					30
Trp	Thr	Thr	Val	Phe	Gln	Gly	Glu	Arg	Val	Thr	Leu	Thr	Cys	Lys
				35					40					45
Gly	Phe	Arg	Phe	Tyr	Ser	Pro	Gln	Lys	Thr	Lys	Trp	Tyr	His	Arg
				50					55					60
Tyr	Leu	Gly	Lys	Glu	Ile	Leu	Arg	Glu	Thr	Pro	Asp	Asn	Ile	Leu
				65					70					75
Glu	Val	Gln	Glu	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	Ala	Gln	Gly	Ser
				80					85					90
Pro	Leu	Ser	Ser	Pro	Val	His	Leu	Asp	Phe	Ser	Ser	Glu	Met	Gly
				95					100					105
Phe	Pro	His	Ala	Ala	Gln	Ala	Asn	Val	Glu	Leu	Leu	Gly	Ser	Ser
				110					115					120

Asp Leu Leu Thr

<210> 147

<211> 1621

<212> DNA

<213> Homo sapiens

<400> 147

cagaagaggg ggctagctag ctgtctctgc ggaccagggg gacccccgcg 50  
 cccccccggt gtgaggcggc ctcacagggc cgggtgggct ggcgagccga 100  
 cgcggcggcg gaggaggctg tgaggagtgt gtggaacagg acccgggaca 150

gaggaacccat ggctccgcag aacctgagca ccttttgcct gttgctgcta 200  
 tacctcatcg gggcgggtgat tgccggacga gatttctata agatcttggg 250  
 ggtgcctcga agtgccctcta taaaggatat taaaaaggcc tataggaaac 300  
 tagccctgca gcttcatccc gaccggaacc ctgatgatcc acaagcccag 350  
 gagaaattcc aggatctggg tgctgcttat gaggttctgt cagatagtga 400  
 gaaacggaaa cagtacgata cttatgggtga agaaggatta aaagatggtc 450  
 atcagagctc ccatggagac attttttcac acttctttgg ggatttttgt 500  
 ttcatgtttg gaggaacccc tcgtcagcaa gacagaaata ttccaagagg 550  
 aagtgatatt attgtagatc tagaagtcac tttggaagaa gtatatgcag 600  
 gaaattttgt ggaagtagtt agaaacaaac ctgtggcaag gcaggctcct 650  
 ggcaaacgga agtgcaattg tcggcaagag atgcggacca cccagctggg 700  
 ccctggggcg ttccaaatga cccaggaggt ggtctgcgac gaatgcccta 750  
 atgtcaaaact agtgaatgaa gaacgaacgc tggaagtaga aatagagcct 800  
 ggggtgagag acggcatgga gtaccctttt attggagaag gtgagcctca 850  
 cgtggatggg gagcctggag atttacggtt ccgaatcaaa gttgtcaagc 900  
 acccaatatt tgaaaggaga ggagatgatt tgtacacaaa tgtgacaatc 950  
 tcattagttg agtcaactgg tggctttgag atggatatta ctcaacttga 1000  
 tggtcacaag gtacatatct cccgggataa gatcaccagg ccaggagcga 1050  
 agctatggaa gaaaggggaa gggctcccca actttgacaa caacaatatc 1100  
 aagggtcttt tgataatcac ttttgatgtg gattttccaa aagaacagtt 1150  
 aacagaggaa gcgagagaag gtatcaaaca gctactgaaa caagggtcag 1200  
 tgcagaaggt atacaatgga ctgcaaggat attgagagtg aataaaattg 1250  
 gactttgttt aaaataagtg aataagcgat atttattatc tgcaaggttt 1300  
 ttttgtgtgt gtttttgttt ttattttcaa tatgcaagtt aggtttaatt 1350  
 tttttatcta atgatcatca tgaaatgaat aagagggcct aagaatttgt 1400  
 ccatttgcat tcggaaaaga atgaccagca aaagggtttac taatacctct 1450  
 cccttggggg atttaatgtc tgggtgctgcc gcctgagttt caagaattaa 1500  
 agctgcaaga ggactccagg agcaaaagaa acacaatata gagggttgga 1550  
 gttgttagca atttcattca aaatgccaac tggagaagtc tgtttttaaa 1600  
 tacattttgt tgttattttt a 1621

<210> 148  
 <211> 358  
 <212> PRT

<213> Homo sapiens

<400> 148

Met	Ala	Pro	Gln	Asn	Leu	Ser	Thr	Phe	Cys	Leu	Leu	Leu	Leu	Tyr
1				5					10					15
Leu	Ile	Gly	Ala	Val	Ile	Ala	Gly	Arg	Asp	Phe	Tyr	Lys	Ile	Leu
				20					25					30
Gly	Val	Pro	Arg	Ser	Ala	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Ala	Tyr
				35					40					45
Arg	Lys	Leu	Ala	Leu	Gln	Leu	His	Pro	Asp	Arg	Asn	Pro	Asp	Asp
				50					55					60
Pro	Gln	Ala	Gln	Glu	Lys	Phe	Gln	Asp	Leu	Gly	Ala	Ala	Tyr	Glu
				65					70					75
Val	Leu	Ser	Asp	Ser	Glu	Lys	Arg	Lys	Gln	Tyr	Asp	Thr	Tyr	Gly
				80					85					90
Glu	Glu	Gly	Leu	Lys	Asp	Gly	His	Gln	Ser	Ser	His	Gly	Asp	Ile
				95					100					105
Phe	Ser	His	Phe	Phe	Gly	Asp	Phe	Gly	Phe	Met	Phe	Gly	Gly	Thr
				110					115					120
Pro	Arg	Gln	Gln	Asp	Arg	Asn	Ile	Pro	Arg	Gly	Ser	Asp	Ile	Ile
				125					130					135
Val	Asp	Leu	Glu	Val	Thr	Leu	Glu	Glu	Val	Tyr	Ala	Gly	Asn	Phe
				140					145					150
Val	Glu	Val	Val	Arg	Asn	Lys	Pro	Val	Ala	Arg	Gln	Ala	Pro	Gly
				155					160					165
Lys	Arg	Lys	Cys	Asn	Cys	Arg	Gln	Glu	Met	Arg	Thr	Thr	Gln	Leu
				170					175					180
Gly	Pro	Gly	Arg	Phe	Gln	Met	Thr	Gln	Glu	Val	Val	Cys	Asp	Glu
				185					190					195
Cys	Pro	Asn	Val	Lys	Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu	Glu	Val
				200					205					210
Glu	Ile	Glu	Pro	Gly	Val	Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe	Ile
				215					220					225
Gly	Glu	Gly	Glu	Pro	His	Val	Asp	Gly	Glu	Pro	Gly	Asp	Leu	Arg
				230					235					240
Phe	Arg	Ile	Lys	Val	Val	Lys	His	Pro	Ile	Phe	Glu	Arg	Arg	Gly
				245					250					255
Asp	Asp	Leu	Tyr	Thr	Asn	Val	Thr	Ile	Ser	Leu	Val	Glu	Ser	Leu
				260					265					270
Val	Gly	Phe	Glu	Met	Asp	Ile	Thr	His	Leu	Asp	Gly	His	Lys	Val
				275					280					285
His	Ile	Ser	Arg	Asp	Lys	Ile	Thr	Arg	Pro	Gly	Ala	Lys	Leu	Trp
				290					295					300

Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys  
 305 310 315  
 Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln  
 320 325 330  
 Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln  
 335 340 345  
 Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr  
 350 355

<210> 149  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445,  
 482  
 <223> unknown base

<400> 149  
 tgggaccagg gaaccccggg ccccccggtg gagngcctaa caggccggtg 50  
 gntgcgaccg aagcggcggg cggaggaggt tttgaggatt tttggaacag 100  
 gaccgggaca gaggaacctt ggttccgcag aacntgagca cnttttgcct 150  
 gttgntgnta tacttcatcg gggcggtgat tgccggagca gatttntata 200  
 agattttggg gtgcctngaa gtgcctnta taaaggatat taaaaaggcc 250  
 tataggaaac tagccctgca gntttatccc gaccggaacc ctgatgatcc 300  
 acaagcccag gagaaattcc aggatttggg tgctgcttat gaggttntgt 350  
 cagatagtga gaaacggaaa cagtacgata attatggtga agaaggatta 400  
 aaagatggtn atcagagctc ccatggagac attttttcac acttntttgg 450  
 ggattttggt ttcattgttg gaggaacccc tngtcagcaa gacagaaata 500  
 ttccaagag 509

<210> 150  
 <211> 1532  
 <212> DNA  
 <213> Homo sapiens

<400> 150  
 ggcacgaggc ggcggggcag tcgcgggatg cgcccgaggag ccacagcctg 50  
 aggccctcag gtctctgcag gtgtcgtgga ggaacctagc acctgccatc 100  
 ctcttcccca atttgccact tccagcagct ttagcccatg aggaggatgt 150  
 gaccgggact gagtcaggag ccctctggaa gcatggagac tgtggtgatt 200  
 gttgccatag gtgtgctggc caccatcttt ctggcttcgt ttgcagcctt 250  
 ggtgctggtt tgcaggcagc gctactgccg gccgcgagac ctgctgcagc 300

gctatgattc taagcccatt gtggacctca ttggtgccat ggagaccag 350  
 tctgagccct ctgagttaga actggacgat gtcgttatca ccaaccccca 400  
 cattgaggcc attctggaga atgaagactg gatcgaagat gcctcgggtc 450  
 tcatgtocca ctgcattgcc atcttgaaga ttgtcacac tctgacagag 500  
 aagcttgttg ccatgacaat gggctctggg gccaatga agacttcagc 550  
 cagtgtcagc gacatcattg tgggtggccaa gcggatcagc cccaggggtg 600  
 atgatgttgt gaagtcgatg taccctccgt tggaccccaa actcctggac 650  
 gcacggacga ctgccctgct cctgtctgtc agtcacctgg tgctggtgac 700  
 aaggaatgcc tgccatctga cgggaggcct ggactggatt gaccagtctc 750  
 tgtcggctgc tgaggagcat ttggaagtcc ttcgagaagc agccctagct 800  
 tctgagccag ataaaggcct cccaggccct gaaggcttcc tgcaggagca 850  
 gtctgcaatt tagtgctac aggccagcag ctagccatga aggccctgc 900  
 cgccatccct ggatggctca gcttagcctt ctactttttc ctatagagtt 950  
 agttgtttct caccgctgga gagttcagct gtgtgtgcat agtaaagcag 1000  
 gagatccccg tcagtttatg cctcttttgc agttgcaaac tgtggctggt 1050  
 gagtggcagt ctaatactac agttagggga gatgccattc actctctgca 1100  
 agaggagtat tgaaaactgg tggactgtca gctttattta gctcacctag 1150  
 tgttttcaag aaaattgagc caccgtctaa gaaatcaaga ggtttcacat 1200  
 taaaattaga atttctggcc tctctcgatc ggtcagaatg tgtggcaatt 1250  
 ctgatctgca ttttcagaag aggacaatca attgaaacta agtaggggtt 1300  
 tcttcttttg gcaagacttg tactctctca cctggcctgt ttcatttatt 1350  
 tgtattatct gcctggctcc tgaggcgtct gggctctctc tctcccttgc 1400  
 aggtttgggt ttgaagctga ggaactacaa agttgatgat ttctttttta 1450  
 tctttatgcc tgcaatttta cctagctacc actaggtgga tagtaaattt 1500  
 atacttatgt ttccctcaaa aaaaaaaaaa aa 1532

<210> 151  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens

<400> 151  
 Met Glu Thr Val Val Ile Val Ala Ile Gly Val Leu Ala Thr Ile  
 1 5 10 15  
 Phe Leu Ala Ser Phe Ala Ala Leu Val Leu Val Cys Arg Gln Arg  
 20 25 30  
 Tyr Cys Arg Pro Arg Asp Leu Leu Gln Arg Tyr Asp Ser Lys Pro

35					40					45				
Ile	Val	Asp	Leu	Ile	Gly	Ala	Met	Glu	Thr	Gln	Ser	Glu	Pro	Ser
				50					55					60
Glu	Leu	Glu	Leu	Asp	Asp	Val	Val	Ile	Thr	Asn	Pro	His	Ile	Glu
				65					70					75
Ala	Ile	Leu	Glu	Asn	Glu	Asp	Trp	Ile	Glu	Asp	Ala	Ser	Gly	Leu
				80					85					90
Met	Ser	His	Cys	Ile	Ala	Ile	Leu	Lys	Ile	Cys	His	Thr	Leu	Thr
				95					100					105
Glu	Lys	Leu	Val	Ala	Met	Thr	Met	Gly	Ser	Gly	Ala	Lys	Met	Lys
				110					115					120
Thr	Ser	Ala	Ser	Val	Ser	Asp	Ile	Ile	Val	Val	Ala	Lys	Arg	Ile
				125					130					135
Ser	Pro	Arg	Val	Asp	Asp	Val	Val	Lys	Ser	Met	Tyr	Pro	Pro	Leu
				140					145					150
Asp	Pro	Lys	Leu	Leu	Asp	Ala	Arg	Thr	Thr	Ala	Leu	Leu	Leu	Ser
				155					160					165
Val	Ser	His	Leu	Val	Leu	Val	Thr	Arg	Asn	Ala	Cys	His	Leu	Thr
				170					175					180
Gly	Gly	Leu	Asp	Trp	Ile	Asp	Gln	Ser	Leu	Ser	Ala	Ala	Glu	Glu
				185					190					195
His	Leu	Glu	Val	Leu	Arg	Glu	Ala	Ala	Leu	Ala	Ser	Glu	Pro	Asp
				200					205					210
Lys	Gly	Leu	Pro	Gly	Pro	Glu	Gly	Phe	Leu	Gln	Glu	Gln	Ser	Ala
				215					220					225

Ile

<210> 152  
 <211> 1027  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 1017, 1020  
 <223> unknown base

<400> 152  
 gcttcatttc tcccgactca gcttcccacc ctgggctttc cgaggtgctt 50  
 tcgccgctgt cccaccact gcagccatga tctccttaac ggacacgcag 100  
 aaaattggaa tgggattaac aggatttgga gtgtttttcc tgttctttgg 150  
 aatgattctc ttttttgaca aagcactact ggctattgga aatgttttat 200  
 ttgtagccgg cttggctttt gtaattgggt tagaaagaac attcagattc 250  
 ttcttccaaa aacataaaat gaaagctaca gggttttttc tgggtggtgt 300

attttagtagtc cttatttggtt ggcctttgat aggcatgatac ttcgaaattt 350  
 atggattttt tctcttggtc aggggcttct ttctgtcgt tgttggttt 400  
 attagaagag tgccagtcct tggatccctc cttaaatttac ctggaattag 450  
 atcatttgta gataaagttg gagaaagcaa caatatggta taacaacaag 500  
 tgaatttgaa gactcattta aaatattgtg ttatttataa agtcatttga 550  
 agaatattca gcacaaaatt aaattacatg aaatagcttg taatgttctt 600  
 tacaggagtt taaaacgtat agcctacaaa gtaccagcag caaattagca 650  
 aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 700  
 caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc 750  
 ttgaaggcta tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc 800  
 ttagagaact gtggtgcctg tttcttttct ttttattttg aaggctcagg 850  
 agcatccata ggcatttgct ttttagaagt gtccactgca atggcaaaaa 900  
 tatttccagt tgcactgtat ctctggaagt gatgcatgaa ttcgattgga 950  
 ttgtgtcatt ttaaagtatt aaaaccaagg aaacccaat tttgatgtat 1000  
 ggattacttt tttttgngcn cagggcc 1027

<210> 153  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> N-myristoylation Sites  
 <222> 11-16, 51-56 and 116-121  
 <223> N-myristoylation Sites.

<220>  
 <221> Transmembrane domains  
 <222> 12-30, 33-52, 69-89 and 93-109  
 <223> Transmembrane domains

<220>  
 <221> Aminoacyl-transfer RNA Synthetases.  
 <222> 49-59  
 <223> Aminoacyl-transfer RNA synthetases class-II protein.

<400> 153  
 Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr  
 1 5 10 15  
 Gly Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe  
 20 25 30  
 Asp Lys Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly  
 35 40 45  
 Leu Ala Phe Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe  
 50 55 60

Gln	Lys	His	Lys	Met	Lys	Ala	Thr	Gly	Phe	Phe	Leu	Gly	Gly	Val
				65					70					75
Phe	Val	Val	Leu	Ile	Gly	Trp	Pro	Leu	Ile	Gly	Met	Ile	Phe	Glu
				80					85					90
Ile	Tyr	Gly	Phe	Phe	Leu	Leu	Phe	Arg	Gly	Phe	Phe	Pro	Val	Val
				95					100					105
Val	Gly	Phe	Ile	Arg	Arg	Val	Pro	Val	Leu	Gly	Ser	Leu	Leu	Asn
				110					115					120
Leu	Pro	Gly	Ile	Arg	Ser	Phe	Val	Asp	Lys	Val	Gly	Glu	Ser	Asn
				125					130					135

Asn Met Val

<210> 154  
 <211> 405  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 66  
 <223> unknown base

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 ttaacgggat ttggagtgtt tttcctgttc tttggaatga ttctcttttt 200  
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 aaaatgaaag ctacaggttt tttctgggt ggtgtatttg tagtccttat 350  
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 <212> DNA  
 <213> Homo sapiens

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 tttcttcctt ctggaaatct ttgactgtgg gtagttattt atttctgaat 150  
 aagagcgtcc acgcatcatg gacctcggg gactgctgaa gtctcagttc 200  
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 cgcgcaagtg ggagcaggat cgcaagacgg ttgccaccag tttgcagcac 650  
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 gctgcagggg agggcagggc tggggaccga aggggacaag ttcccccttc 1650  
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<210> 156

<211> 378  
<212> PRT  
<213> Homo sapiens

<400> 156

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				20					25					30	
Ile	Gln	Leu	Phe	Thr	Leu	Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	
				35					40					45	
Phe	Arg	Lys	Ile	Asn	Cys	Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	
				50					55					60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	
				65					70					75	
Phe	Thr	Asp	Pro	Arg	Ala	Tyr	Leu	Lys	Tyr	Gly	Lys	Glu	Asn	Ala	
				80					85					90	
Ile	Val	Val	Leu	Asn	His	Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	
				95					100					105	
Trp	Ser	Leu	Ser	Glu	Arg	Phe	Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	
				110					115					120	
Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp	Met	
				125					130					135	
Trp	Tyr	Phe	Thr	Glu	Met	Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln	
				140					145					150	
Asp	Arg	Lys	Thr	Val	Ala	Thr	Ser	Leu	Gln	His	Leu	Arg	Asp	Tyr	
				155					160					165	
Pro	Glu	Lys	Tyr	Phe	Phe	Leu	Ile	His	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Lys	Lys	His	Glu	Ile	Ser	Met	Gln	Val	Ala	Arg	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Arg	Leu	Lys	His	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Ala	Ile	Thr	Val	Arg	Ser	Leu	Arg	Asn	Val	Val	Ser	Ala	Val	
				215					220					225	
Tyr	Asp	Cys	Thr	Leu	Asn	Phe	Arg	Asn	Asn	Glu	Asn	Pro	Thr	Leu	
				230					235					240	
Leu	Gly	Val	Leu	Asn	Gly	Lys	Lys	Tyr	His	Ala	Asp	Leu	Tyr	Val	
				245					250					255	
Arg	Arg	Ile	Pro	Leu	Glu	Asp	Ile	Pro	Glu	Asp	Asp	Asp	Glu	Cys	
				260					265					270	
Ser	Ala	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Phe	Gln	
				275					280					285	
Glu	Glu	Tyr	Tyr	Arg	Thr	Gly	Thr	Phe	Pro	Glu	Thr	Pro	Met	Val	

290	295	300
Pro Pro Arg Arg Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala		
305	310	315
Ser Leu Val Leu Tyr Pro Phe Phe Gln Phe Leu Val Ser Met Ile		
320	325	330
Arg Ser Gly Ser Ser Leu Thr Leu Ala Ser Phe Ile Leu Val Phe		
335	340	345
Phe Val Ala Ser Val Gly Val Arg Trp Met Ile Gly Val Thr Glu		
350	355	360
Ile Asp Lys Gly Ser Ala Tyr Gly Asn Ser Asp Ser Lys Gln Lys		
365	370	375

Leu Asn Asp

<210> 157  
 <211> 1849  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
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 tactgattcc caaatggatg atgttgaagt tgtttataca attgacattc 200  
 agaaatatat tccatgctat cagcttttta gcttttataa ttcttcaggc 250  
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 gaccttggtt ttctgctatt aacaccaagt ataataacag aaagctgctc 450  
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 acaaacacac agctctaaat tttttgaaga agatggatcc tttaaaggagg 650  
 tacataagat aaatgaaatg tatgcttcat tacaagagga attaaagagt 700  
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actacaacca ccatctcgat gtagtagaca atctgacctt aatggtagaa 1000  
 cactactgaca ttcttgaagc tagtccagct agtacaccac aaatcattaa 1050  
 gcataaagcc ttagacttag atgacagatg gcaattcaag agatctcggg 1100  
 tgtagatac acaagacaaa cgatctaaag caaatactgg tagtagtaac 1150  
 caagataaag catccaaaat gagcagccca gaaacagatg aagaaattga 1200  
 aaagatgaag gggtttggtg aatattcacg gtctcctaca ttttgatcct 1250  
 ttttaacctta caaggagatt tttttatttg gctgatgggt aaagccaaac 1300  
 atttctattg tttttactat gttgagctac ttgcagtaag ttcatttggt 1350  
 tttactatgt tcacctgttt gcagtaatac acagataact cttagtgcat 1400  
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 tttttttcac ctttactaa gttgttgagg ggaaggctta cacagacaca 1500  
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 tgaaaattta tctgagtcac taaaattctc cttaagtcat acttttttag 1750  
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 aaatttgcaa aacatcatct aaaattttaaa aaaaaaaaaa aaaaaaaaaa 1849

<210> 158  
 <211> 409  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
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 Gly Phe Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile  
 35 40 45  
 Thr Asp Ser Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp  
 50 55 60  
 Ile Gln Lys Tyr Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn  
 65 70 75  
 Ser Ser Gly Glu Val Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser  
 80 85 90  
 Asn Val Lys Lys Asn Val Val Gly Trp Tyr Lys Phe Arg Arg His  
 95 100 105

Ser Asp Gln Ile	Met Thr Phe Arg Glu	Arg Leu Leu His Lys	Asn
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Leu Gln Glu His	Phe Ser Asn Gln Asp	Leu Val Phe Leu Leu	Leu
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Thr Pro Ser Ile	Ile Thr Glu Ser Cys	Ser Thr His Arg Leu	Glu
140		145	150
His Ser Leu Tyr	Lys Pro Gln Lys Gly	Leu Phe His Arg Val	Pro
155		160	165
Leu Val Val Ala	Asn Leu Gly Met Ser	Glu Gln Leu Gly Tyr	Lys
170		175	180
Thr Val Ser Gly	Ser Cys Met Ser Thr	Gly Phe Ser Arg Ala	Val
185		190	195
Gln Thr His Ser	Ser Lys Phe Phe Glu	Glu Asp Gly Ser Leu	Lys
200		205	210
Glu Val His Lys	Ile Asn Glu Met Tyr	Ala Ser Leu Gln Glu	Glu
215		220	225
Leu Lys Ser Ile	Cys Lys Lys Val Glu	Asp Ser Glu Gln Ala	Val
230		235	240
Asp Lys Leu Val	Lys Asp Val Asn Arg	Leu Lys Arg Glu Ile	Glu
245		250	255
Lys Arg Arg Gly	Ala Gln Ile Gln Ala	Ala Arg Glu Lys Asn	Ile
260		265	270
Gln Lys Asp Pro	Gln Glu Asn Ile Phe	Leu Cys Gln Ala Leu	Arg
275		280	285
Thr Phe Phe Pro	Asn Ser Glu Phe Leu	His Ser Cys Val Met	Ser
290		295	300
Leu Lys Asn Arg	His Val Ser Lys Ser	Ser Cys Asn Tyr Asn	His
305		310	315
His Leu Asp Val	Val Asp Asn Leu Thr	Leu Met Val Glu His	Thr
320		325	330
Asp Ile Pro Glu	Ala Ser Pro Ala Ser	Thr Pro Gln Ile Ile	Lys
335		340	345
His Lys Ala Leu	Asp Leu Asp Asp Arg	Trp Gln Phe Lys Arg	Ser
350		355	360
Arg Leu Leu Asp	Thr Gln Asp Lys Arg	Ser Lys Ala Asn Thr	Gly
365		370	375
Ser Ser Asn Gln	Asp Lys Ala Ser Lys	Met Ser Ser Pro Glu	Thr
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395		400	405
Ser Pro Thr Phe			

<210> 159  
<211> 2651  
<212> DNA  
<213> Homo sapiens

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<210> 160  
 <211> 556  
 <212> PRT  
 <213> Homo sapiens

<400> 160  
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 Ser Glu Val Arg Arg Leu Tyr Val Ser Lys Gly Phe Asn Lys Asn

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Pro	Gln	Gly	Ser	Thr	Cys	Cys	Ser	Gln	Glu	Met	Glu	Glu	Lys	Tyr
				65										75
Ser	Leu	Gln	Ser	Lys	Asp	Asp	Phe	Lys	Ser	Val	Val	Ser	Glu	Gln
				80										90
Cys	Asn	His	Leu	Gln	Ala	Val	Phe	Ala	Ser	Arg	Tyr	Lys	Lys	Phe
				95										105
Asp	Glu	Phe	Phe	Lys	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu
				110										120
Asn	Asp	Met	Phe	Val	Lys	Thr	Tyr	Gly	His	Leu	Tyr	Met	Gln	Asn
				125										135
Ser	Glu	Leu	Phe	Lys	Asp	Leu	Phe	Val	Glu	Leu	Lys	Arg	Tyr	Tyr
				140										150
Val	Val	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp
				155										165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Arg	Leu	Val	Asn	Ser	Gln	Tyr
				170										180
His	Phe	Thr	Asp	Glu	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Glu
				185										195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Leu	Gln
				200										210
Val	Thr	Arg	Ala	Phe	Val	Ala	Ala	Arg	Thr	Phe	Ala	Gln	Gly	Leu
				215										225
Ala	Val	Ala	Gly	Asp	Val	Val	Ser	Lys	Val	Ser	Val	Val	Asn	Pro
				230										240
Thr	Ala	Gln	Cys	Thr	His	Ala	Leu	Leu	Lys	Met	Ile	Tyr	Cys	Ser
				245										255
His	Cys	Arg	Gly	Leu	Val	Thr	Val	Lys	Pro	Cys	Tyr	Asn	Tyr	Cys
				260										270
Ser	Asn	Ile	Met	Arg	Gly	Cys	Leu	Ala	Asn	Gln	Gly	Asp	Leu	Asp
				275										285
Phe	Glu	Trp	Asn	Asn	Phe	Ile	Asp	Ala	Met	Leu	Met	Val	Ala	Glu
				290										300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile
				305										315
Asp	Val	Lys	Ile	Ser	Asp	Ala	Ile	Met	Asn	Met	Gln	Asp	Asn	Ser
				320										330
Val	Gln	Val	Ser	Gln	Lys	Val	Phe	Gln	Gly	Cys	Gly	Pro	Pro	Lys
				335										345
Pro	Leu	Pro	Ala	Gly	Arg	Ile	Ser	Arg	Ser	Ile	Ser	Glu	Ser	Ala

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Phe	Ser	Ala	Arg	Phe	Arg	Pro	His	His	Pro	Glu	Glu	Arg	Pro	Thr
				365					370					375
Thr	Ala	Ala	Gly	Thr	Ser	Leu	Asp	Arg	Leu	Val	Thr	Asp	Val	Lys
				380					385					390
Glu	Lys	Leu	Lys	Gln	Ala	Lys	Lys	Phe	Trp	Ser	Ser	Leu	Pro	Ser
				395					400					405
Asn	Val	Cys	Asn	Asp	Glu	Arg	Met	Ala	Ala	Gly	Asn	Gly	Asn	Glu
				410					415					420
Asp	Asp	Cys	Trp	Asn	Gly	Lys	Gly	Lys	Ser	Arg	Tyr	Leu	Phe	Ala
				425					430					435
Val	Thr	Gly	Asn	Gly	Leu	Ala	Asn	Gln	Gly	Asn	Asn	Pro	Glu	Val
				440					445					450
Gln	Val	Asp	Thr	Ser	Lys	Pro	Asp	Ile	Leu	Ile	Leu	Arg	Gln	Ile
				455					460					465
Met	Ala	Leu	Arg	Val	Met	Thr	Ser	Lys	Met	Lys	Asn	Ala	Tyr	Asn
				470					475					480
Gly	Asn	Asp	Val	Asp	Phe	Phe	Asp	Ile	Ser	Asp	Glu	Ser	Ser	Gly
				485					490					495
Glu	Gly	Ser	Gly	Ser	Gly	Cys	Glu	Tyr	Gln	Gln	Cys	Pro	Ser	Glu
				500					505					510
Phe	Asp	Tyr	Asn	Ala	Thr	Asp	His	Ala	Gly	Lys	Ser	Ala	Asn	Glu
				515					520					525
Lys	Ala	Asp	Ser	Ala	Gly	Val	Arg	Pro	Gly	Ala	Gln	Ala	Tyr	Leu
				530					535					540
Leu	Thr	Val	Phe	Cys	Ile	Leu	Phe	Leu	Val	Met	Gln	Arg	Glu	Trp
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<210> 161

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 161

ctccgtggtta aacccccacag ccc 23

<210> 162

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 162  
tcacatcgat gggatccatg accg 24

<210> 163  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 163  
ggtctcgtga ctgtgaagcc atgttacaac tactgctcaa acatcatgag 50

<210> 164  
<211> 870  
<212> DNA  
<213> Homo sapiens

<400> 164  
ctcgccctca aatgggaacg ctggcctggg actaaagcat agaccaccag 50  
gctgagtatc ctgacctgag tcatccccag ggatcaggag cctccagcag 100  
ggaaccttcc attatattct tcaagcaact tacagctgca cgcacagttg 150  
cgatgaaagt tctaattctt tccctcctcc tgttgctgcc actaatgctg 200  
atgtccatgg tctctagcag cctgaatcca ggggtcgcca gaggccacag 250  
ggaccgaggc caggcttcta ggagatggct ccaggaaggc ggccaagaat 300  
gtgagtgcaa agattggttc ctgagagccc cgagaagaaa attcatgaca 350  
gtgtctgggc tgccaaagaa gcagtgcgcc tgtgatcatt tcaagggcaa 400  
tgtgaagaaa acaagacacc aaaggcacca cagaaagcca aacaagcatt 450  
ccagagcctg ccagcaattt ctcaaacaat gtcagctaag aagctttgct 500  
ctgcctttgt aggagctctg agcgcccact cttccaatta aacatttctca 550  
gccaagaaga cagtgagcac acctaccaga cactcttctt ctcccacctc 600  
actctcccac tgtaccaccc cctaaatcat tccagtgtc tcaaaaagca 650  
tgtttttcaa gatcattttg tttgttgctc tctctagtgt cttcttctct 700  
cgtcagtctt agcctgtgcc ctccccttac ccaggcttag gcttaattac 750  
ctgaaagatt ccaggaaaact gtagcttctt agctagtgtc atttaacctt 800  
aatgcaatc aggaaagtag caaacagaag tcaataaata tttttaaatg 850  
tcaaaaaaaaa aaaaaaaaaa 870

<210> 165  
<211> 119  
<212> PRT  
<213> Homo sapiens

<400> 165  
Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Pro Leu Met

1	5	10	15
Leu Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg	20	25	30
Gly His Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu	35	40	45
Gly Gly Gln Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro	50	55	60
Arg Arg Lys Phe Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys	65	70	75
Pro Cys Asp His Phe Lys Gly Asn Val Lys Lys Thr Arg His Gln	80	85	90
Arg His His Arg Lys Pro Asn Lys His Ser Arg Ala Cys Gln Gln	95	100	105
Phe Leu Lys Gln Cys Gln Leu Arg Ser Phe Ala Leu Pro Leu	110	115	

<210> 166  
 <211> 551  
 <212> DNA  
 <213> Homo sapiens

<400> 166  
 aatggctgtc ttagtacttc gcctgacagt tgtcctggga ctgcttgtct 50  
 tattcctgac ctgctatgca gacgacaaac cagacaagcc agacgacaag 100  
 ccagacgact cgggcaaaga cccaaagcca gacttcccca aattcctaag 150  
 cctcctgggc acagagatca ttgagaatgc agtcgagttc atcctccgct 200  
 ccatgtccag gagcacagga tttatggaat ttgatgataa tgaaggaaaa 250  
 cattcatcaa agtgacatcc tcaggacaca cccatgtggc tcctggacaa 300  
 tccaagagca gccaaatcct gcttttccag tttggctcca caagtcctcc 350  
 aggacagagc cctcaaagca actcccaacg agttctcagg attcaggctc 400  
 tggcttcaac caaacagaac tcattttgaa caccctgact gcatttttgc 450  
 ttttagaaaag ttagaataaa tatggcgctt tgggatcaca tagttgatgg 500  
 agaggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550  
 a 551

<210> 167  
 <211> 87  
 <212> PRT  
 <213> Homo sapiens

<400> 167  
 Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu  
 1 5 10 15  
 Val Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro

	20		25		30
Asp Asp Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe					
	35		40		45
Pro Lys Phe Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala					
	50		55		60
Val Glu Phe Ile Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met					
	65		70		75
Glu Phe Asp Asp Asn Glu Gly Lys His Ser Ser Lys					
	80		85		

<210> 168  
 <211> 1371  
 <212> DNA  
 <213> Homo sapiens

<400> 168  
 ggacgccagc gcctgcagag gctgagcagg gaaaaagcca gtgccccagc 50  
 ggaagcacag ctcagagctg gtctgccatg gacatccttg tcccactcct 100  
 gcagctgctg gtgctgcttc ttaccctgcc cctgcacctc atggctctgc 150  
 tgggctgctg gcagcccctg tgcaaaagct acttccccta cctgatggcc 200  
 gtgctgactc ccaagagcaa ccgcaagatg gagagcaaga aacgggagct 250  
 cttcagccag ataaaggggc ttacaggagc ctccgggaaa gtggccctac 300  
 tggagctggg ctgcggaacc ggagccaact ttcagttcta cccaccgggc 350  
 tgcaggggtca cctgcctaga cccaaatccc cactttgaga agttcctgac 400  
 aaagagcatg gctgagaaca ggcacctcca atatgagcgg tttgtggtgg 450  
 ctcttgagga ggacatgaga cagctggctg atggctccat ggatgtggtg 500  
 gtctgcactc tgggtgctgtg ctctgtgcag agcccaagga aggtcctgca 550  
 ggaggtccgg agagtactga gaccgggagg tgtgctcttt ttctggggagc 600  
 atgtggcaga accatatgga agctgggcct tcatgtggca gcaagttttc 650  
 gagcccacct ggaaacacat tggggatggc tgctgcctca ccagagagac 700  
 ctggaaggat cttgagaacg cccagttctc cgaaatccaa atggaacgac 750  
 agccccctcc cttgaagtgg ctacctgttg ggccccacat catgggaaag 800  
 gctgtcaaac aatctttccc aagctccaag gcactcattt gctccttccc 850  
 cagcctccaa ttagaacaag ccaccaccca gcctatctat cttccactga 900  
 gagggaccta gcagaatgag agaagacatt catgtaccac ctactagtcc 950  
 ctctctcccc aacctctgcc agggcaatct ctaacttcaa tcccgcttc 1000  
 gacagtgaag aagctctact tctacgctga ccagggagg aaacactagg 1050  
 accctgttgt atcctcaact gcaagtttct ggactagtct cccaacgttt 1100

gcctcccaat gttgtccctt tccttcgttc ccatggtaaa gtcctctctg 1150  
 ctttcctcct gaggtacac ccatgctgtct ctaggaactg gtcacaaaag 1200  
 tcatggtgcc tgcacccctg ccaagccccc ctgaccctct ctccccacta 1250  
 ccaccttctt cctgagctgg gggcaccagg gagaatcaga gatgctgggg 1300  
 atgccagagc aagactcaaa gaggcagagg ttttgttctc aaatattttt 1350  
 taataaatag acgaaaccac g 1371

<210> 169  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 169  
 Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu  
 1 5 10 15  
 Thr Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro  
 20 25 30  
 Leu Cys Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro  
 35 40 45  
 Lys Ser Asn Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser  
 50 55 60  
 Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu  
 65 70 75  
 Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro  
 80 85 90  
 Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His Phe Glu Lys  
 95 100 105  
 Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln Tyr Glu  
 110 115 120  
 Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala Asp  
 125 130 135  
 Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val  
 140 145 150  
 Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg  
 155 160 165  
 Pro Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr  
 170 175 180  
 Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp  
 185 190 195  
 Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys  
 200 205 210  
 Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln  
 215 220 225

Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly  
 230 235 240

Lys Ala Val Lys Gln Ser Phe Pro Ser Ser Lys Ala Leu Ile Cys  
 245 250 255

Ser Phe Pro Ser Leu Gln Leu Glu Gln Ala Thr His Gln Pro Ile  
 260 265 270

Tyr Leu Pro Leu Arg Gly Thr  
 275

<210> 170  
 <211> 1621  
 <212> DNA  
 <213> Homo sapiens

<400> 170  
 gtgggattta tttgagtgc agatcgtttt ctcagtgggtg gtggaagttg 50  
 cctcatcgca ggcagatggt ggggctttgt ccgaacagct cccctctgcc 100  
 agcttctgta gataagggtt aaaaactaat atttatatga cagaagaaaa 150  
 agatgtcatt ccgtaaagta aacatcatca tcttggtcct ggctgttgct 200  
 ctcttcttac tggttttgca ccataacttc ctgagcttga gcagtttggt 250  
 aaggaatgag gttacagatt caggaattgt agggcctcaa cctatagact 300  
 ttgtcccaaa tgctctccga catgcagtag atgggagaca agaggagatt 350  
 cctgtgggtca tcgctgcac tgaagacagg cttggggggg ccattgcagc 400  
 tataaacagc attcagcaca aactcgctc caatgtgatt ttctacattg 450  
 ttactctcaa caatacagca gaccatctcc ggtcctggct caacagtgat 500  
 tccctgaaaa gcatcagata caaaattgtc aattttgacc ctaaactttt 550  
 ggaaggaaaa gtaaaggagg atcctgacca gggggaatcc atgaaacctt 600  
 taacctttgc aaggttctac ttgccaatc tgggtcccag cgcaaagaag 650  
 gccatataca tggatgatga tgtaattgtg caaggtgata ttcttgccct 700  
 ttacaataca gcactgaagc caggacatgc agctgcattt tcagaagatt 750  
 gtgattcagc ctctactaaa gttgtcatcc gtggagcagg aaaccagtac 800  
 aattacattg gctatcttga ctataaaaag gaaagaattc gtaagctttc 850  
 catgaaagcc agcatttgc catttaatcc tggagttttt gttgcaaacc 900  
 tgacggaatg gaaacgacag aatataacta accaactgga aaaatggatg 950  
 aaactcaatg tagaagaggg actgtatagc agaaccctgg ctggtagcat 1000  
 cacaacacct cctctgctta tcgtatttta tcaacagcac tctaccatcg 1050  
 atcctatgtg gaatgtccgc cacottgggt ccagtgtctg aaaacgatat 1100  
 tcacctcagt ttgtaaaggc tgccaagtta ctccattgga atggacattt 1150

gaagccatgg ggaaggactg cttcatatac tgatgtttgg gaaaaatggt 1200  
atattccaga cccaacaggc aaattcaacc taatccgaag atataccgag 1250  
atctcaaaca taaagtgaaa cagaatttga actgtaagca agcattttctc 1300  
aggaagtcct ggaagatagc atgcatggga agtaacagtt gctaggcttc 1350  
aatgcctatc ggtagcaagc catggaaaaa gatgtgtcag ctaggtaaaag 1400  
atgacaaact gccctgtctg gcagtcagct tcccagacag actatagact 1450  
ataaatatgt ctccatctgc cttaccaagt gttttcttac tacaatgctg 1500  
aatgactgga aagaagaact gatatggcta gttcagctag ctggtacaga 1550  
taattcaaaa ctgctgttgg ttttaatttt gtaacctgtg gccatgatctg 1600  
taaataaaaac ttacatTTTT c 1621

<210> 171  
<211> 371  
<212> PRT  
<213> Homo sapiens

<400> 171  
Met Ser Phe Arg Lys Val Asn Ile Ile Ile Leu Val Leu Ala Val  
1 5 10 15  
Ala Leu Phe Leu Leu Val Leu His His Asn Phe Leu Ser Leu Ser  
20 25 30  
Ser Leu Leu Arg Asn Glu Val Thr Asp Ser Gly Ile Val Gly Pro  
35 40 45  
Gln Pro Ile Asp Phe Val Pro Asn Ala Leu Arg His Ala Val Asp  
50 55 60  
Gly Arg Gln Glu Glu Ile Pro Val Val Ile Ala Ala Ser Glu Asp  
65 70 75  
Arg Leu Gly Gly Ala Ile Ala Ala Ile Asn Ser Ile Gln His Asn  
80 85 90  
Thr Arg Ser Asn Val Ile Phe Tyr Ile Val Thr Leu Asn Asn Thr  
95 100 105  
Ala Asp His Leu Arg Ser Trp Leu Asn Ser Asp Ser Leu Lys Ser  
110 115 120  
Ile Arg Tyr Lys Ile Val Asn Phe Asp Pro Lys Leu Leu Glu Gly  
125 130 135  
Lys Val Lys Glu Asp Pro Asp Gln Gly Glu Ser Met Lys Pro Leu  
140 145 150  
Thr Phe Ala Arg Phe Tyr Leu Pro Ile Leu Val Pro Ser Ala Lys  
155 160 165  
Lys Ala Ile Tyr Met Asp Asp Asp Val Ile Val Gln Gly Asp Ile  
170 175 180  
Leu Ala Leu Tyr Asn Thr Ala Leu Lys Pro Gly His Ala Ala Ala

185	190	195
Phe Ser Glu Asp Cys Asp Ser Ala Ser	Thr Lys Val Val Ile Arg	
200	205	210
Gly Ala Gly Asn Gln Tyr Asn Tyr Ile	Gly Tyr Leu Asp Tyr Lys	
215	220	225
Lys Glu Arg Ile Arg Lys Leu Ser Met	Lys Ala Ser Thr Cys Ser	
230	235	240
Phe Asn Pro Gly Val Phe Val Ala Asn	Leu Thr Glu Trp Lys Arg	
245	250	255
Gln Asn Ile Thr Asn Gln Leu Glu Lys	Trp Met Lys Leu Asn Val	
260	265	270
Glu Glu Gly Leu Tyr Ser Arg Thr Leu	Ala Gly Ser Ile Thr Thr	
275	280	285
Pro Pro Leu Leu Ile Val Phe Tyr Gln	Gln His Ser Thr Ile Asp	
290	295	300
Pro Met Trp Asn Val Arg His Leu Gly	Ser Ser Ala Gly Lys Arg	
305	310	315
Tyr Ser Pro Gln Phe Val Lys Ala Ala	Lys Leu Leu His Trp Asn	
320	325	330
Gly His Leu Lys Pro Trp Gly Arg Thr	Ala Ser Tyr Thr Asp Val	
335	340	345
Trp Glu Lys Trp Tyr Ile Pro Asp Pro	Thr Gly Lys Phe Asn Leu	
350	355	360
Ile Arg Arg Tyr Thr Glu Ile Ser Asn	Ile Lys	
365	370	

<210> 172  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 71, 76, 86, 91, 162, 220, 269, 281  
 <223> unknown base

<400> 172  
 tggtttttgc cccataaatt ccctcagctt gagcagtttg ttaaggaatg 50  
 aggttacaga ttcaggaatt ntaggnccctc aacctntaga ntttgtccca 100  
 aatgtttotcc gacatgcagt agatgggaga caagaggaga ttcctgtggt 150  
 catcgctgca tntgaagaca ggcttggggg ggccattgca gctataaaca 200  
 gcattcagca caacaactcgn tccaatgtga ttttctacat tgttactctc 250  
 aacaatacag cagaccatnt ccggtcctgg ntcaacagtg attccctgaa 300  
 aagcatcaga tacaaaattg tcaattttga ccctaaactt ttggaaggaa 350

aagtaaagga ggatcctgac cagggggaat ccatgaaacc tttaaccttt 400  
gcaaggttct acttgccaat tctggttccc agcgcaaaga aggccatata 450  
catggatgat gatgtaattg tgcaagggtga tattcttgcc ctttacaata 500  
cagcaactgaa gccaggacat gcagctgcat tttcagaaga ttgtgattca 550  
gcctctacta aagttgtcat ccgtggagca ggaaa 585

<210> 173  
<211> 1866  
<212> DNA  
<213> Homo sapiens

<400> 173  
cgacgctcta gcggttaccg ctgcgggctg gctgggcgta gtggggctgc 50  
gcggctgcca cggagctaga gggcaagtgt gctcgccca gcgtgcaggg 100  
aacgcgggcg gccagacaac gggctgggct ccggggcctg cggcgcgggc 150  
gctgagctgg cagggcggggt cggggcgcgg gctgcatcog catctcctcc 200  
atcgccctgca gtaagggcgg ccgcggcgag cctttgaggg gaacgacttg 250  
tcggagccct aaccaggggt gtctctgagc ctggtgggat ccccgagcg 300  
tcacatcact ttccgatcac ttcaaagtgg ttaaaaacta atatttatat 350  
gacagaagaa aaagatgtca ttccgtaaag taaacatcat catcttggtc 400  
ctgggctgtt gctctcttct tactggtttt gcaccataac ttcttcagct 450  
tgaggcagtt tgtaagga tgagggtaca gattcaggaa ttgtagggcc 500  
tcaacctata ggactttgtc ccaaatgctc tccgacatgc agtagatggg 550  
agacaagagg agattcctgt ggtcatcgct gcactgaag acaggcttgg 600  
gggggccatt gcagctataa acagcattca gcacaacact cgctccaatg 650  
tgattttcta cattgttact ctcaacaata cagcagacca tctccggtcc 700  
tgggctcaac agtgattccc tgaaaagcat cagatacaaa attgtcaatt 750  
ttgaccctaa acttttgga ggaaggtaa aggaggatcc tgaccagggg 800  
gaatccatga aacctttaac ctttgcaagg ttctacttgc caattctggg 850  
ttcccagcgc aaagaaggcc atatacatgg atgatgatgt aattgtgcaa 900  
ggatgatattc ttgcccttta caatacagca ctgaagccag gacatgcagc 950  
tgcattttca gaagattgtg attcagcctc tactaaagt gtcatccgtg 1000  
gagcaggaaa ccagtacaat tacattggct atcttgacta taaaaaggaa 1050  
agaattcgta agctttccat gaaagccagc acttgctcat ttaatcctgg 1100  
agtttttgtt gcaaacctga cggaatggaa acgacagaat ataactaacc 1150  
aactggaaaa atggatgaaa ctcaatgtag aagagggact gtatagcaga 1200

accctggctg gtagcatcac aacacotcct ctgcttatcg tattttatca 1250  
 acagcactct accatcgatc ctatgtggaa tgtccgccac cttgggtcca 1300  
 gtgctggaaa acgatattca cctcagtttg taaaggctgc caagttactc 1350  
 cattggaatg gacatttgaa gccatgggga aggactgctt catatactga 1400  
 tgtttgggga aaaatggtat attccagacc caacaggcaa attcaaccta 1450  
 atccgaagat ataccgagat ctcaaacata aagtgaacaa gaatttgaac 1500  
 tgtaagcaag cattttctcag gaagtccctgg aagatagcat gcgtgggaag 1550  
 taacagttgc taggcttcaa tgcctatcgg tagcaagcca tggaaaaaga 1600  
 tgtgtcagct aggtaaagat gacaaactgc cctgtctggc agtcagcttc 1650  
 ccagacagac tatagactat aaatatgtct ccatctgcct taccaagtgt 1700  
 ttcttacta caatgctgaa tgactggaaa gaagaactga tatggctagt 1750  
 tcagctagct ggtacagata attcaaaact gctgttggtt ttaattttgt 1800  
 aacctgtggc ctgatctgta aataaaactt acatttttca ataggtaaaa 1850  
 aaaaaaaaa aaaaaa 1866

<210> 174  
 <211> 823  
 <212> DNA  
 <213> Homo sapiens

<400> 174  
 ctgcaggtag acatctccac tgcccaggaa tcaactgagcg tgcagacagc 50  
 acagcctcct ctgaaggccg gccataccag agtcctgcct cggcatgggc 100  
 ctcaccattg aggagctcc actgtctgtg ctggtctgag ggtgctgcct 150  
 gtcattggggg cagccatctc ccagggggcc ctcatcgcca tcgtctgcaa 200  
 cggctctctg ggcttcttgc tgctgctgct ctgggtcctc ctctgctggg 250  
 cctgccattc tcgtctgccg acgttgactc tctctctgaa tccagtccca 300  
 actccagccc tggccctgt cctgagaagg cccaccacc ccagaagccc 350  
 agccatgaag gcagctacct gctgcagccc tgaaggcccc tggcctagcc 400  
 tggagcccag gacctaagtc cacctcacct agagcctgga attaggatcc 450  
 cagagttcag ccagcctggg gtccagaact caagagtccg cctgcttgga 500  
 gctggaccca gcggcccaga gtctagccag cttgggtcca ataggagctc 550  
 agtggcccta aggagatggg cctgggggtg gggcttatga gttggtgcta 600  
 gagccagggc catctggact atgctccatc ccaagggcca agggtcaggg 650  
 gccgggtcca ctctttccct aggtgagca cctctaggcc ctctaggttg 700  
 gggaagcaaa ctggaaccca tggcaataat aggaggggtg ccaggctggg 750

ccccctccctt ggctctccca gtgtttgctg gataataaat ggaactatgg 800

ctctaaaaaa aaaaaaaaaa aaa 823

<210> 175

<211> 87

<212> PRT

<213> Homo sapiens

<400> 175

Met Gly Ala Ala Ile Ser Gln Gly Ala Leu Ile Ala Ile Val Cys  
1 5 10 15

Asn Gly Leu Val Gly Phe Leu Leu Leu Leu Leu Trp Val Ile Leu  
20 25 30

Cys Trp Ala Cys His Ser Arg Leu Pro Thr Leu Thr Leu Ser Leu  
35 40 45

Asn Pro Val Pro Thr Pro Ala Leu Ala Pro Val Leu Arg Arg Pro  
50 55 60

His His Pro Arg Ser Pro Ala Met Lys Ala Ala Thr Cys Cys Ser  
65 70 75

Pro Glu Gly Pro Trp Pro Ser Leu Glu Pro Arg Thr  
80 85

<210> 176

<211> 1660

<212> DNA

<213> Homo sapiens

<400> 176

gtttgaattc cttcaactat acccacagtc caaaagcaga ctcaactgtgt 50

cccaggctac cagttcctcc aagcaagtca tttcccttat ttaaccgatg 100

tgtccctcaa acacctgagt gctactccct atttgcatct gttttgataa 150

atgatgttga caccctccac cgaattctaa gtggaatcat gtcgggaaga 200

gatacaatcc ttggcctgtg tatcctcgca ttagccttgt ctttggccat 250

gatgtttacc ttcagattca tcaccaccct tctgggtcac attttcattt 300

cattggttat tttgggattg ttgtttgtct gcggtgtttt atggtggctg 350

tattatgact ataccaacga cctcagcata gaattggaca cagaaaggga 400

aaatatgaag tgcgtgctgg gggttgctat cgtatccaca ggcacacgg 450

cagtgtgtct cgtcttgatt tttgtttctca gaaagagaat aaaattgaca 500

gttgagcttt tccaaatcac aaataaagcc atcagcagtg ctcccttcct 550

gctgttccag ccactgtgga catttgccat cctcattttc ttctgggtcc 600

tctgggtggc tgtgctgctg agcctgggaa ctgcaggagc tgcccaggtt 650

atggaaggcg gccaaagtga atataagccc ctttcgggca ttcggtacat 700

gtggctgtac catttaattg gcctcatctg gactagtga ttcattcctt 750

cgtgccagca aatgactata gctggggcag tggttacttg ttatttcaac 800  
 agaagtaaaa atgatoctcc tgatcatccc atcctttcgt ctctctccat 850  
 tctcttcttc taccatcaag gaaccgttgt gaaaggttca tttttaatct 900  
 ctgtggtgag gattccgaga atcattgtca tgtacatgca aaacgcactg 950  
 aaagaacagc agcatggtgc attgtccagg tacctgttcc gatgctgcta 1000  
 ctgctgtttc tgggtgtcttg acaaatacct gctccatctc aaccagaatg 1050  
 catatactac aactgctatt aatgggacag atttctgtac atcagcaaaa 1100  
 gatgcattca aaatcttgtc caagaactca agtcacttta catctattaa 1150  
 ctgcttttga gacttcataa tttttctagg aaaggtgtta gtggtgtgtt 1200  
 tcaactgtttt tggaggactc atggccttta actacaatcg ggcattccag 1250  
 gtgtgggcag tccctctgtt attggtagct ttttttgcct acttagtagc 1300  
 ccatagtttt ttatctgtgt ttgaaactgt gctggatgca cttttcctgt 1350  
 gttttgctgt tgatctggaa acaaatgatg gatcgtcaga aaagccctac 1400  
 tttatggatc aagaatttct gagtttcgta aaaaggagca acaaattaaa 1450  
 caatgcaagg gcacagcagg acaagcactc attaaggaat gaggagggaa 1500  
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 <212> PRT  
 <213> Homo sapiens

<400> 177  
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 Leu Leu Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu  
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 Phe Val Cys Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn  
 50 55 60  
 Asp Leu Ser Ile Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys  
 65 70 75  
 Val Leu Gly Phe Ala Ile Val Ser Thr Gly Ile Thr Ala Val Leu  
 80 85 90  
 Leu Val Leu Ile Phe Val Leu Arg Lys Arg Ile Lys Leu Thr Val

95										100					105				
Glu	Leu	Phe	Gln	Ile	Thr	Asn	Lys	Ala	Ile	Ser	Ser	Ala	Pro	Phe					
				110					115					120					
Leu	Leu	Phe	Gln	Pro	Leu	Trp	Thr	Phe	Ala	Ile	Leu	Ile	Phe	Phe					
				125					130					135					
Trp	Val	Leu	Trp	Val	Ala	Val	Leu	Leu	Ser	Leu	Gly	Thr	Ala	Gly					
				140					145					150					
Ala	Ala	Gln	Val	Met	Glu	Gly	Gly	Gln	Val	Glu	Tyr	Lys	Pro	Leu					
				155					160					165					
Ser	Gly	Ile	Arg	Tyr	Met	Trp	Ser	Tyr	His	Leu	Ile	Gly	Leu	Ile					
				170					175					180					
Trp	Thr	Ser	Glu	Phe	Ile	Leu	Ala	Cys	Gln	Gln	Met	Thr	Ile	Ala					
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Gly	Ala	Val	Val	Thr	Cys	Tyr	Phe	Asn	Arg	Ser	Lys	Asn	Asp	Pro					
				200					205					210					
Pro	Asp	His	Pro	Ile	Leu	Ser	Ser	Leu	Ser	Ile	Leu	Phe	Phe	Tyr					
				215					220					225					
His	Gln	Gly	Thr	Val	Val	Lys	Gly	Ser	Phe	Leu	Ile	Ser	Val	Val					
				230					235					240					
Arg	Ile	Pro	Arg	Ile	Ile	Val	Met	Tyr	Met	Gln	Asn	Ala	Leu	Lys					
				245					250					255					
Glu	Gln	Gln	His	Gly	Ala	Leu	Ser	Arg	Tyr	Leu	Phe	Arg	Cys	Cys					
				260					265					270					
Tyr	Cys	Cys	Phe	Trp	Cys	Leu	Asp	Lys	Tyr	Leu	Leu	His	Leu	Asn					
				275					280					285					
Gln	Asn	Ala	Tyr	Thr	Thr	Thr	Ala	Ile	Asn	Gly	Thr	Asp	Phe	Cys					
				290					295					300					
Thr	Ser	Ala	Lys	Asp	Ala	Phe	Lys	Ile	Leu	Ser	Lys	Asn	Ser	Ser					
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His	Phe	Thr	Ser	Ile	Asn	Cys	Phe	Gly	Asp	Phe	Ile	Ile	Phe	Leu					
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Gly	Lys	Val	Leu	Val	Val	Cys	Phe	Thr	Val	Phe	Gly	Gly	Leu	Met					
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Ala	Phe	Asn	Tyr	Asn	Arg	Ala	Phe	Gln	Val	Trp	Ala	Val	Pro	Leu					
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Leu	Leu	Val	Ala	Phe	Phe	Ala	Tyr	Leu	Val	Ala	His	Ser	Phe	Leu					
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Ser	Val	Phe	Glu	Thr	Val	Leu	Asp	Ala	Leu	Phe	Leu	Cys	Phe	Ala					
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Val	Asp	Leu	Glu	Thr	Asn	Asp	Gly	Ser	Ser	Glu	Lys	Pro	Tyr	Phe					
				395					400					405					
Met	Asp	Gln	Glu	Phe	Leu	Ser	Phe	Val	Lys	Arg	Ser	Asn	Lys	Leu					

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Glu Gly Thr Glu Leu Gln Ala Ile Val Arg		
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 <212> DNA  
 <213> Homo sapiens

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 caatcgttat cctaccacg atggagagaa tcctttatcg tcttagaaaag 600  
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 cgaaaagtcc agctgcccaa gcaggtgaga ccacaaaagc ctatcagagg 700  
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 ggctgtcact gtagctgtgg ccacccccac caccttgcca aggccatccc 800  
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 aaagaagaat tgagcacaca gtctttggag ccagtatccc tgggagatcc 1050  
 aaactgcaaa attgacttgt cgtttttaat tgatgggagc accagcattg 1100  
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<210> 179

<211> 678  
 <212> PRT  
 <213> Homo sapiens

<400> 179

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Ala	Lys	Lys	Ile	Lys	Arg	Pro	Lys	Phe	Thr	Val	Pro	Gln	Ile	Asn	35	40	45	
Cys	Asp	Val	Lys	Ala	Gly	Lys	Ile	Ile	Asp	Pro	Glu	Phe	Ile	Val	50	55	60	
Lys	Cys	Pro	Ala	Gly	Cys	Gln	Asp	Pro	Lys	Tyr	His	Val	Tyr	Gly	65	70	75	
Thr	Asp	Val	Tyr	Ala	Ser	Tyr	Ser	Ser	Val	Cys	Gly	Ala	Ala	Val	80	85	90	
His	Ser	Gly	Val	Leu	Asp	Asn	Ser	Gly	Gly	Lys	Ile	Leu	Val	Arg	95	100	105	
Lys	Val	Ala	Gly	Gln	Ser	Gly	Tyr	Lys	Gly	Ser	Tyr	Ser	Asn	Gly	110	115	120	
Val	Gln	Ser	Leu	Ser	Leu	Pro	Arg	Trp	Arg	Glu	Ser	Phe	Ile	Val	125	130	135	
Leu	Glu	Ser	Lys	Pro	Lys	Lys	Gly	Val	Thr	Tyr	Pro	Ser	Ala	Leu	140	145	150	
Thr	Tyr	Ser	Ser	Ser	Lys	Ser	Pro	Ala	Ala	Gln	Ala	Gly	Glu	Thr	155	160	165	
Thr	Lys	Ala	Tyr	Gln	Arg	Pro	Pro	Ile	Pro	Gly	Thr	Thr	Ala	Gln	170	175	180	
Pro	Val	Thr	Leu	Met	Gln	Leu	Leu	Ala	Val	Thr	Val	Ala	Val	Ala	185	190	195	
Thr	Pro	Thr	Thr	Leu	Pro	Arg	Pro	Ser	Pro	Ser	Ala	Ala	Ser	Thr	200	205	210	
Thr	Ser	Ile	Pro	Arg	Pro	Gln	Ser	Val	Gly	His	Arg	Ser	Gln	Glu	215	220	225	
Met	Asp	Leu	Trp	Ser	Thr	Ala	Thr	Tyr	Thr	Ser	Ser	Gln	Asn	Arg	230	235	240	
Pro	Arg	Ala	Asp	Pro	Gly	Ile	Gln	Arg	Gln	Asp	Pro	Ser	Gly	Ala	245	250	255	
Ala	Phe	Gln	Lys	Pro	Val	Gly	Ala	Asp	Val	Ser	Leu	Gly	Leu	Val	260	265	270	
Pro	Lys	Glu	Glu	Leu	Ser	Thr	Gln	Ser	Leu	Glu	Pro	Val	Ser	Leu	275	280	285	
Gly	Asp	Pro	Asn	Cys	Lys	Ile	Asp	Leu	Ser	Phe	Leu	Ile	Asp	Gly				

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Ser	Thr	Ser	Ile	Gly	Lys	Arg	Arg	Phe	Arg	Ile	Gln	Lys	Gln	Leu					
				305					310					315					
Leu	Ala	Asp	Val	Ala	Gln	Ala	Leu	Asp	Ile	Gly	Pro	Ala	Gly	Pro					
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Leu	Met	Gly	Val	Val	Gln	Tyr	Gly	Asp	Asn	Pro	Ala	Thr	His	Phe					
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Asn	Leu	Lys	Thr	His	Thr	Asn	Ser	Arg	Asp	Leu	Lys	Thr	Ala	Ile					
				350					355					360					
Glu	Lys	Ile	Thr	Gln	Arg	Gly	Gly	Leu	Ser	Asn	Val	Gly	Arg	Ala					
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Ile	Ser	Phe	Val	Thr	Lys	Asn	Phe	Phe	Ser	Lys	Ala	Asn	Gly	Asn					
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Arg	Ser	Gly	Ala	Pro	Asn	Val	Val	Val	Val	Met	Val	Asp	Gly	Trp					
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Pro	Thr	Asp	Lys	Val	Glu	Glu	Ala	Ser	Arg	Leu	Ala	Arg	Glu	Ser					
				410					415					420					
Gly	Ile	Asn	Ile	Phe	Phe	Ile	Thr	Ile	Glu	Gly	Ala	Ala	Glu	Asn					
				425					430					435					
Glu	Lys	Gln	Tyr	Val	Val	Glu	Pro	Asn	Phe	Ala	Asn	Lys	Ala	Val					
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Cys	Arg	Thr	Asn	Gly	Phe	Tyr	Ser	Leu	His	Val	Gln	Ser	Trp	Phe					
				455					460					465					
Gly	Leu	His	Lys	Thr	Leu	Gln	Pro	Leu	Val	Lys	Arg	Val	Cys	Asp					
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Thr	Asp	Arg	Leu	Ala	Cys	Ser	Lys	Thr	Cys	Leu	Asn	Ser	Ala	Asp					
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Ile	Gly	Phe	Val	Ile	Asp	Gly	Ser	Ser	Ser	Val	Gly	Thr	Gly	Asn					
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Phe	Arg	Thr	Val	Leu	Gln	Phe	Val	Thr	Asn	Leu	Thr	Lys	Glu	Phe					
				515					520					525					
Glu	Ile	Ser	Asp	Thr	Asp	Thr	Arg	Ile	Gly	Ala	Val	Gln	Tyr	Thr					
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Tyr	Glu	Gln	Arg	Leu	Glu	Phe	Gly	Phe	Asp	Lys	Tyr	Ser	Ser	Lys					
				545					550					555					
Pro	Asp	Ile	Leu	Asn	Ala	Ile	Lys	Arg	Val	Gly	Tyr	Trp	Ser	Gly					
				560					565					570					
Gly	Thr	Ser	Thr	Gly	Ala	Ala	Ile	Asn	Phe	Ala	Leu	Glu	Gln	Leu					
				575					580					585					
Phe	Lys	Lys	Ser	Lys	Pro	Asn	Lys	Arg	Lys	Leu	Met	Ile	Leu	Ile					
				590					595					600					
Thr	Asp	Gly	Arg	Ser	Tyr	Asp	Asp	Val	Arg	Ile	Pro	Ala	Met	Ala					

	605		610		615
Ala His Leu Lys	Gly Val Ile Thr Tyr	Ala Ile Gly Val Ala	Trp		
	620	625	630		
Ala Ala Gln Glu	Glu Leu Glu Val Ile	Ala Thr His Pro Ala	Arg		
	635	640	645		
Asp His Ser Phe	Phe Val Asp Glu Phe	Asp Asn Leu His Gln	Tyr		
	650	655	660		
Val Pro Arg Ile	Ile Gln Asn Ile Cys	Thr Glu Phe Asn Ser	Gln		
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Pro Arg Asn

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 <211> 1759  
 <212> DNA  
 <213> Homo sapiens

<400> 180  
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 gcgctgctgc ctacgaccca tggcgccca ggtcccgcgc gctccgcgcc 150  
 agatcccgcc cactacagtt tttctctgac tctaattgat gcaactggaca 200  
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 aacaaacatt cgagtggtag gaggactcct gtctgctcat ctgctctcca 350  
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 atcataaaa 1759

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 <211> 541  
 <212> PRT  
 <213> Homo sapiens

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 Asp Pro Ala His Tyr Ser Phe Ser Leu Thr Leu Ile Asp Ala Leu  
 35 40 45  
 Asp Thr Leu Leu Ile Leu Gly Asn Val Ser Glu Phe Gln Arg Val  
 50 55 60  
 Val Glu Val Leu Gln Asp Ser Val Asp Phe Asp Ile Asp Val Asn  
 65 70 75  
 Ala Ser Val Phe Glu Thr Asn Ile Arg Val Val Gly Gly Leu Leu  
 80 85 90  
 Ser Ala His Leu Leu Ser Lys Lys Ala Gly Val Glu Val Glu Ala  
 95 100 105  
 Gly Trp Pro Cys Ser Gly Pro Leu Leu Arg Met Ala Glu Glu Ala  
 110 115 120  
 Ala Arg Lys Leu Leu Pro Ala Phe Gln Thr Pro Thr Gly Met Pro

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Pro	Val	Thr	Cys	Thr	Ala	Gly	Ile	Gly	Thr	Phe	Ile	Val	Glu	Phe					
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Ala	Thr	Leu	Ser	Ser	Leu	Thr	Gly	Asp	Pro	Val	Phe	Glu	Asp	Val					
				170					175					180					
Ala	Arg	Val	Ala	Leu	Met	Arg	Leu	Trp	Glu	Ser	Arg	Ser	Asp	Ile					
				185					190					195					
Gly	Leu	Val	Gly	Asn	His	Ile	Asp	Val	Leu	Thr	Gly	Lys	Trp	Val					
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Ala	Gln	Asp	Ala	Gly	Ile	Gly	Ala	Gly	Val	Asp	Ser	Tyr	Phe	Glu					
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Tyr	Leu	Val	Lys	Gly	Ala	Ile	Leu	Leu	Gln	Asp	Lys	Lys	Leu	Met					
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Ala	Met	Phe	Leu	Glu	Tyr	Asn	Lys	Ala	Ile	Arg	Asn	Tyr	Thr	Arg					
				245					250					255					
Phe	Asp	Asp	Trp	Tyr	Leu	Trp	Val	Gln	Met	Tyr	Lys	Gly	Thr	Val					
				260					265					270					
Ser	Met	Pro	Val	Phe	Gln	Ser	Leu	Glu	Ala	Tyr	Trp	Pro	Gly	Leu					
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Gln	Ser	Leu	Ile	Gly	Asp	Ile	Asp	Asn	Ala	Met	Arg	Thr	Phe	Leu					
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Asn	Tyr	Tyr	Thr	Val	Trp	Lys	Gln	Phe	Gly	Gly	Leu	Pro	Glu	Phe					
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Tyr	Asn	Ile	Pro	Gln	Gly	Tyr	Thr	Val	Glu	Lys	Arg	Glu	Gly	Tyr					
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Pro	Leu	Arg	Pro	Glu	Leu	Ile	Glu	Ser	Ala	Met	Tyr	Leu	Tyr	Arg					
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Ala	Thr	Gly	Asp	Pro	Thr	Leu	Leu	Glu	Leu	Gly	Arg	Asp	Ala	Val					
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Glu	Ser	Ile	Glu	Lys	Ile	Ser	Lys	Val	Glu	Cys	Gly	Phe	Ala	Thr					
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Ile	Lys	Asp	Leu	Arg	Asp	His	Lys	Leu	Asp	Asn	Arg	Met	Glu	Ser					
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Phe	Phe	Leu	Ala	Glu	Thr	Val	Lys	Tyr	Leu	Tyr	Leu	Leu	Phe	Asp					
				395					400					405					
Pro	Thr	Asn	Phe	Ile	His	Asn	Asn	Gly	Ser	Thr	Phe	Asp	Ala	Val					
				410					415					420					
Ile	Thr	Pro	Tyr	Gly	Glu	Cys	Ile	Leu	Gly	Ala	Gly	Gly	Tyr	Ile					
				425					430					435					
Phe	Asn	Thr	Glu	Ala	His	Pro	Ile	Asp	Leu	Ala	Ala	Leu	His	Cys					

440	445	450
Cys Gln Arg Leu Lys Glu Glu Gln Trp Glu Val Glu Asp Leu Met		
455	460	465
Arg Glu Phe Tyr Ser Leu Lys Arg Ser Arg Ser Lys Phe Gln Lys		
470	475	480
Asn Thr Val Ser Ser Gly Pro Trp Glu Pro Pro Ala Arg Pro Gly		
485	490	495
Thr Leu Phe Ser Pro Glu Asn His Asp Gln Ala Arg Glu Arg Lys		
500	505	510
Pro Ala Lys Gln Lys Val Pro Leu Leu Ser Cys Pro Ser Gln Pro		
515	520	525
Phe Thr Ser Lys Leu Ala Leu Leu Gly Gln Val Phe Leu Asp Ser		
530	535	540

Ser

<210> 182  
 <211> 2056  
 <212> DNA  
 <213> Homo sapiens

<400> 182  
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 gcttctctggg ccggtcttag aacaattcag gcttcgctgc gactcagacc 150  
 tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
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 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000  
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 aaaaaa 2056

<210> 183

<211> 311

<212> PRT

<213> Homo sapiens

<220>

<221> Signal peptide

<222> 1-29

<223> Signal peptide

<220>

<221> N-glycosylation sites

<222> 40-43, 134-137

<223> N-glycosylation sites.

<220>

<221> Tissue factor proteins homology

<222> 92-119

<223> Tissue factor proteins homology

<220>

<221> Transmembrane domain

<222> 230-255

<223> Transmembrane domain

<220>

<221> Integrins alpha chain protein homology

<222> 232-262

<223> Integrins alpha chain protein homology

<400> 183

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Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp	
				20					25					30	
Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	
				35					40					45	
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	
				50					55					60	
Gly	Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	
				65					70					75	
Ser	Leu	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	
				80					85					90	
Leu	Thr	Glu	Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	
				95					100					105	
Thr	Val	Pro	Tyr	Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	
				110					115					120	
Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	
				125					130					135	
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	
				140					145					150	
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	
				155					160					165	
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	
				170					175					180	
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	
				185					190					195	
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	
				200					205					210	
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	
				215					220					225	

Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe
				230					235					240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp
				245					250					255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val
				260					265					270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile
				275					280					285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met
				290					295					300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser				
				305					310					

<210> 184  
 <211> 808  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 654, 711, 748  
 <223> unknown base

<400> 184  
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 tagacotcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
 agaatgcttt attttgaaa gaaacaatgt tctaggtaa actgagtcta 200  
 ccaaagtcag actttcaca tggttctaga agaaatctgg acaagtcttt 250  
 tcatgtggtt tttctacgca ttgattccat gtttgcac agatgaagt 300  
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350  
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
 attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450  
 tggatcccca gcagctggtg ctcaactcact gaaggtcctg agtgtgatgt 500  
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcc 550  
 cattgggctc acagacctca gcctggagca tctgaagca tccctttaat 600  
 agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650  
 cttncacctg gttattgagc tggaggacct ggggcccag tttgagttcc 700  
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
 gaacctcttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800  
 tgaccac 808

<210> 185  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
aggcttcgct gcgactagac ctc 23

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
ccaggtcggg taaggatggt tgag 24

<210> 187  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 188  
<211> 1227  
<212> DNA  
<213> Homo sapiens

<400> 188  
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ggcagcggcg tggctgctcc tgtgggtgc gccctgcgcg cagcaggagc 100  
aggacttcta cgacttcaag gcggtcaaca tcgggggcaa actggtgtcg 150  
ctggagaagt accgcggatc ggtgtccctg gtggtgaatg tggccagcga 200  
gtgcggcttc acagaccagc actaccgagc cctgcagcag ctgcagcgag 250  
acctggggccc ccaccacttt aacgtgctcg ccttccoctg caaccagttt 300  
ggccaacagg agcctgacag caacaaggag attgagagct ttgccgcgcg 350  
cacctacagt gtctattcc ccatgtttag caagattgca gtcaccggtg 400  
ctggtgccc a tctgccttc aagtacctgg ccagacttc tgggaaggag 450  
cccacctgga acttctggaa gtacctagta gcccagatg gaaaggtggt 500  
aggggcttgg gacccaactg tgctcagtga ggaggtcaga cccagatca 550  
cagcgtcgt gaggaagctc atcctactga agcgagaaga cttataacca 600

ccgcgtctcc tctccacca cctcatcccg cccacctgtg tggggctgac 650  
 caatgcaaac tcaaattggtg cttcaaaggg agagaccac tgactctcct 700  
 tcttttactc ttatgccatt ggtcccatca ttcttgtggg ggaaaaattc 750  
 tagtattttg attatttgaa tcttacagca acaaatagga actcctggcc 800  
 aatgagagct cttgaccagt gaatcaccag ccgatacgaa cgtcttgcca 850  
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 attaggatga aatacctgtg aaagtgccta ggcaagtcca gccaaatagg 1000  
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 caataaaaaac ttgcatccaa catgaatttc cagccgatga taatccaggc 1100  
 caaaggttta gttgttggtta tttcctctgt attattttct tcattacaaa 1150  
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 taaaaatgaa agtatcctcc tcaaaaa 1227

<210> 189  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

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 Val Asn Ile Arg Gly Lys Leu Val Ser Leu Glu Lys Tyr Arg Gly  
 35 40 45  
 Ser Val Ser Leu Val Val Asn Val Ala Ser Glu Cys Gly Phe Thr  
 50 55 60  
 Asp Gln His Tyr Arg Ala Leu Gln Gln Leu Gln Arg Asp Leu Gly  
 65 70 75  
 Pro His His Phe Asn Val Leu Ala Phe Pro Cys Asn Gln Phe Gly  
 80 85 90  
 Gln Gln Glu Pro Asp Ser Asn Lys Glu Ile Glu Ser Phe Ala Arg  
 95 100 105  
 Arg Thr Tyr Ser Val Ser Phe Pro Met Phe Ser Lys Ile Ala Val  
 110 115 120  
 Thr Gly Thr Gly Ala His Pro Ala Phe Lys Tyr Leu Ala Gln Thr  
 125 130 135  
 Ser Gly Lys Glu Pro Thr Trp Asn Phe Trp Lys Tyr Leu Val Ala  
 140 145 150  
 Pro Asp Gly Lys Val Val Gly Ala Trp Asp Pro Thr Val Ser Val

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Glu Glu Val Arg Pro Gln Ile Thr Ala Leu Val Arg Lys Leu Ile			
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Leu Leu Lys Arg Glu Asp Leu			
	185		

<210> 190  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 190  
 gcaggacttc tacgacttca aggc 24

<210> 191  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 191  
 agtctgggcc aggtacttga aggc 24

<210> 192  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 192  
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<210> 193  
 <211> 2187  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
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 ctggggggccc gggccgccct ctctcgaggt tggcaggaag ccaggttgca 150  
 ggggtgtccgc ttctcagtt ccagagaggt ggatcgcgatg gtctccacgc 200  
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 aactcaagga ggaggtggac aaagctgctt ctggcctcct gagcattggc 400

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 gcccotttgc cggggaccct gctcctggat gaagtgggtg cggctggcag 750  
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 aagggggcca ccctotccca ctacaacatt gtcaacaact ccaacatttt 900  
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 ccctcctgtc catccccac attccctgt ctgtccttgt gatttggcat 2150  
 aaagagcttc tgttttcttt gaaaaaaaaa aaaaaaa 2187

<210> 194  
 <211> 615  
 <212> PRT  
 <213> Homo sapiens

<400> 194

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Trp	Gln	Glu	Ala	Arg	Leu	Gln	Gly	Val	Arg	Phe	Leu	Ser	Ser	Arg	35	40	45	
Glu	Val	Asp	Arg	Met	Val	Ser	Thr	Pro	Ile	Gly	Gly	Leu	Ser	Tyr	50	55	60	
Val	Gln	Gly	Cys	Thr	Lys	Lys	His	Leu	Asn	Ser	Lys	Thr	Val	Gly	65	70	75	
Gln	Cys	Leu	Glu	Thr	Thr	Ala	Gln	Arg	Val	Pro	Glu	Arg	Glu	Ala	80	85	90	
Leu	Val	Val	Leu	His	Glu	Asp	Val	Arg	Leu	Thr	Phe	Ala	Gln	Leu	95	100	105	
Lys	Glu	Glu	Val	Asp	Lys	Ala	Ala	Ser	Gly	Leu	Leu	Ser	Ile	Gly	110	115	120	
Leu	Cys	Lys	Gly	Asp	Arg	Leu	Gly	Met	Trp	Gly	Pro	Asn	Ser	Tyr	125	130	135	
Ala	Trp	Val	Leu	Met	Gln	Leu	Ala	Thr	Ala	Gln	Ala	Gly	Ile	Ile	140	145	150	
Leu	Val	Ser	Val	Asn	Pro	Ala	Tyr	Gln	Ala	Met	Glu	Leu	Glu	Tyr	155	160	165	
Val	Leu	Lys	Lys	Val	Gly	Cys	Lys	Ala	Leu	Val	Phe	Pro	Lys	Gln	170	175	180	
Phe	Lys	Thr	Gln	Gln	Tyr	Tyr	Asn	Val	Leu	Lys	Gln	Ile	Cys	Pro	185	190	195	
Glu	Val	Glu	Asn	Ala	Gln	Pro	Gly	Ala	Leu	Lys	Ser	Gln	Arg	Leu	200	205	210	
Pro	Asp	Leu	Thr	Thr	Val	Ile	Ser	Val	Asp	Ala	Pro	Leu	Pro	Gly	215	220	225	
Thr	Leu	Leu	Leu	Asp	Glu	Val	Val	Ala	Ala	Gly	Ser	Thr	Arg	Gln	230	235	240	
His	Leu	Asp	Gln	Leu	Gln	Tyr	Asn	Gln	Gln	Phe	Leu	Ser	Cys	His				

245										250					255				
Asp	Pro	Ile	Asn	Ile	Gln	Phe	Thr	Ser	Gly	Thr	Thr	Gly	Ser	Pro					
				260					265					270					
Lys	Gly	Ala	Thr	Leu	Ser	His	Tyr	Asn	Ile	Val	Asn	Asn	Ser	Asn					
				275					280					285					
Ile	Leu	Gly	Glu	Arg	Leu	Lys	Leu	His	Glu	Lys	Thr	Pro	Glu	Gln					
				290					295					300					
Leu	Arg	Met	Ile	Leu	Pro	Asn	Pro	Leu	Tyr	His	Cys	Leu	Gly	Ser					
				305					310					315					
Val	Ala	Gly	Thr	Met	Met	Cys	Leu	Met	Tyr	Gly	Ala	Thr	Leu	Ile					
				320					325					330					
Leu	Ala	Ser	Pro	Ile	Phe	Asn	Gly	Lys	Lys	Ala	Leu	Glu	Ala	Ile					
				335					340					345					
Ser	Arg	Glu	Arg	Gly	Thr	Phe	Leu	Tyr	Gly	Thr	Pro	Thr	Met	Phe					
				350					355					360					
Val	Asp	Ile	Leu	Asn	Gln	Pro	Asp	Phe	Ser	Ser	Tyr	Asp	Ile	Ser					
				365					370					375					
Thr	Met	Cys	Gly	Gly	Val	Ile	Ala	Gly	Ser	Pro	Ala	Pro	Pro	Glu					
				380					385					390					
Leu	Ile	Arg	Ala	Ile	Ile	Asn	Lys	Ile	Asn	Met	Lys	Asp	Leu	Val					
				395					400					405					
Val	Ala	Tyr	Gly	Thr	Thr	Glu	Asn	Ser	Pro	Val	Thr	Phe	Ala	His					
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Phe	Pro	Glu	Asp	Thr	Val	Glu	Gln	Lys	Ala	Glu	Ser	Val	Gly	Arg					
				425					430					435					
Ile	Met	Pro	His	Thr	Glu	Ala	Arg	Ile	Met	Asn	Met	Glu	Ala	Gly					
				440					445					450					
Thr	Leu	Ala	Lys	Leu	Asn	Thr	Pro	Gly	Glu	Leu	Cys	Ile	Arg	Gly					
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Tyr	Cys	Val	Met	Leu	Gly	Tyr	Trp	Gly	Glu	Pro	Gln	Lys	Thr	Glu					
				470					475					480					
Glu	Ala	Val	Asp	Gln	Asp	Lys	Trp	Tyr	Trp	Thr	Gly	Asp	Val	Ala					
				485					490					495					
Thr	Met	Asn	Glu	Gln	Gly	Phe	Cys	Lys	Ile	Val	Gly	Arg	Ser	Lys					
				500					505					510					
Asp	Met	Ile	Ile	Arg	Gly	Gly	Glu	Asn	Ile	Tyr	Pro	Ala	Glu	Leu					
				515					520					525					
Glu	Asp	Phe	Phe	His	Thr	His	Pro	Lys	Val	Gln	Glu	Val	Gln	Val					
				530					535					540					
Val	Gly	Val	Lys	Asp	Asp	Arg	Met	Gly	Glu	Glu	Ile	Cys	Ala	Cys					
				545					550					555					
Ile	Arg	Leu	Lys	Asp	Gly	Glu	Glu	Thr	Thr	Val	Glu	Glu	Ile	Lys					

	560		565		570
Ala Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr					
	575		580		585
Ile Val Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile					
	590		595		600
Gln Lys Phe Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu					
	605		610		615

<210> 195  
 <211> 642  
 <212> DNA  
 <213> Homo sapiens

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 gtggcaggca caatgatgtg tctgatgtac ggtgccaccc tcatcctggc 150  
 ctctcccatc ttcaatggca agaaggcact ggaggccatc agcagagaga 200  
 gaggcacctt cctgtatggt acccccacga tgttcgtgga cattctgaac 250  
 cagccagact tctccagtta tgacatctcg accatgtgtg gaggtgtcat 300  
 tgctgggtcc cctgcacctc cagagttgat ccgagccatc atcaacaaga 350  
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 gtgacattcg cgcacttccc tgaggacact gtggagcaga aggcagaaag 450  
 cgtgggcaga attatgcctc acacggaggc gcggatcatg aacatggagg 500  
 cagggacgct ggcaaagctg aacacgcccg gggagctgtg catccgaggg 550  
 tactgctca tgctgggcta ctggggtgag cctcagaaga cagaggaagc 600  
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<210> 196  
 <211> 1575  
 <212> DNA  
 <213> Homo sapiens

<400> 196  
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 gatctggact gcaggctggc tgctgctgct gctgcttcgc ggaggagcgc 100  
 aggccctgga gtgctacagc tgcgtgcaga aagcagatga cggatgctcc 150  
 ccgaacaaga tgaagacagt gaagtgcgcg cggggcgtgg acgtctgcac 200  
 cgaggccgtg ggggcggtgg agaccatcca cggacaattc tcgctggcag 250  
 tgccggggtt cggttcggga ctccccggca agaataaccg cggcctggat 300  
 cttcacgggc ttctggcgtt catccagctg cagcaatgcg ctcaggatcg 350

ctgcaacgcc aagctcaacc tcacctcgcg ggcgctcgac ccggcaggta 400  
 atgagagtgc ataccgcgcc aacggcggtg agtgctacag ctgtgtgggc 450  
 ctgagccggg aggcgtgccg ggggtacatcg ccgcccgtcg tgagctgcta 500  
 caacgccagc gatcatgtct acaagggctg cttcgacggc aacgtcacct 550  
 tgacggcagc taatgtgact gtgtccttgc ctgtccgggg ctgtgtccag 600  
 gatgaattct gcaactcgga tggagtaaca ggcccagggt tcacgctcag 650  
 tggctcctgt tgccaggggt cccgctgtaa ctctgacctc cgcaacaaga 700  
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 cccacgactg tggcctcaac cacatctgtc accacttcta cctcggcccc 800  
 agtgagaccc acatccacca ccaaaccat gccagcgcca accagtcaga 850  
 ctccgagaca gggagtagaa cacgaggcct cccgggatga ggagcccagg 900  
 ttgactggag gcgcgcgtgg ccaccaggac cgcagcaatt cagggcagta 950  
 tcttgcaaaa ggggggcccc agcagcccca taataaaggc tgtgtggctc 1000  
 ccacagctgg attggcagcc cttctgttgg ccgtggctgc tgggtgtccta 1050  
 ctgtgagctt ctccacctgg aaatttccct ctccactact tctctggccc 1100  
 tgggtacccc tcttctcatc acttctgtt cccaccactg gactgggctg 1150  
 gccagcccc tgtttttcca acattcccca gtatccccag cttctgctgc 1200  
 gctggtttgc ggctttggga aataaaatac cgttgatat attctgccag 1250  
 ggggtgttcta gctttttgag gacagctcct gtatccttct catccttgtc 1300  
 tctccgcttg tctcttgtg atgttaggac agagtgagag aagtcagctg 1350  
 tcacggggaa ggtgagagag aggatgctaa gcttctact cactttctcc 1400  
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 ctctaagcac tgccctccct actccccgca tctttgggga atcggttccc 1500  
 catatgtctt cttactaga ctgtgagctc ctcgaggggg ggcccgggtac 1550  
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<210> 197

<211> 346

<212> PRT

<213> Homo sapiens

<400> 197

Met	Asp	Pro	Ala	Arg	Lys	Ala	Gly	Ala	Gln	Ala	Met	Ile	Trp	Thr
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Ala	Gly	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Gly	Gly	Ala	Gln	Ala
			20						25					30

Leu	Glu	Cys	Tyr	Ser	Cys	Val	Gln	Lys	Ala	Asp	Asp	Gly	Cys	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45				
Pro	Asn	Lys	Met	Lys	Thr	Val	Lys	Cys	Ala	Pro	Gly	Val	Asp	Val
				50					55					60
Cys	Thr	Glu	Ala	Val	Gly	Ala	Val	Glu	Thr	Ile	His	Gly	Gln	Phe
				65					70					75
Ser	Leu	Ala	Val	Arg	Gly	Cys	Gly	Ser	Gly	Leu	Pro	Gly	Lys	Asn
				80					85					90
Asp	Arg	Gly	Leu	Asp	Leu	His	Gly	Leu	Leu	Ala	Phe	Ile	Gln	Leu
				95					100					105
Gln	Gln	Cys	Ala	Gln	Asp	Arg	Cys	Asn	Ala	Lys	Leu	Asn	Leu	Thr
				110					115					120
Ser	Arg	Ala	Leu	Asp	Pro	Ala	Gly	Asn	Glu	Ser	Ala	Tyr	Pro	Pro
				125					130					135
Asn	Gly	Val	Glu	Cys	Tyr	Ser	Cys	Val	Gly	Leu	Ser	Arg	Glu	Ala
				140					145					150
Cys	Gln	Gly	Thr	Ser	Pro	Pro	Val	Val	Ser	Cys	Tyr	Asn	Ala	Ser
				155					160					165
Asp	His	Val	Tyr	Lys	Gly	Cys	Phe	Asp	Gly	Asn	Val	Thr	Leu	Thr
				170					175					180
Ala	Ala	Asn	Val	Thr	Val	Ser	Leu	Pro	Val	Arg	Gly	Cys	Val	Gln
				185					190					195
Asp	Glu	Phe	Cys	Thr	Arg	Asp	Gly	Val	Thr	Gly	Pro	Gly	Phe	Thr
				200					205					210
Leu	Ser	Gly	Ser	Cys	Cys	Gln	Gly	Ser	Arg	Cys	Asn	Ser	Asp	Leu
				215					220					225
Arg	Asn	Lys	Thr	Tyr	Phe	Ser	Pro	Arg	Ile	Pro	Pro	Leu	Val	Arg
				230					235					240
Leu	Pro	Pro	Pro	Glu	Pro	Thr	Thr	Val	Ala	Ser	Thr	Thr	Ser	Val
				245					250					255
Thr	Thr	Ser	Thr	Ser	Ala	Pro	Val	Arg	Pro	Thr	Ser	Thr	Thr	Lys
				260					265					270
Pro	Met	Pro	Ala	Pro	Thr	Ser	Gln	Thr	Pro	Arg	Gln	Gly	Val	Glu
				275					280					285
His	Glu	Ala	Ser	Arg	Asp	Glu	Glu	Pro	Arg	Leu	Thr	Gly	Gly	Ala
				290					295					300
Ala	Gly	His	Gln	Asp	Arg	Ser	Asn	Ser	Gly	Gln	Tyr	Pro	Ala	Lys
				305					310					315
Gly	Gly	Pro	Gln	Gln	Pro	His	Asn	Lys	Gly	Cys	Val	Ala	Pro	Thr
				320					325					330
Ala	Gly	Leu	Ala	Ala	Leu	Leu	Leu	Ala	Val	Ala	Ala	Gly	Val	Leu
				335					340					345

Leu

<210> 198  
<211> 1657  
<212> DNA  
<213> Homo sapiens

<400> 198  
cgggactcgg cggggtcctcc tgggagtcctc ggaggggacc ggctgtgcag 50  
acgccatgga gttggtgctg gtcttcctct gcagcctgct gggcccatg 100  
gtcctggcca gtgcagctga aaaggagaag gaaatggacc cttttcatta 150  
tgattaccag accctgagga ttgggggact ggtgttcgct gtggtcctct 200  
tctcggttgg gatcctcctt atcctaagtc gcaggtgcaa gtgcagtttc 250  
aatcagaagc cccgggcccc aggagatgag gaagcccagg tggagaacct 300  
catcaccgcc aatgcaacag agccccagaa gcagagaact gaagtgcagc 350  
catcagggtgg aagcctctgg aacctgaggc ggctgcttga acctttggat 400  
gcaaagtgtg atgcttaaga aaaccggcca cttcagcaac agccctttcc 450  
ccaggagaag ccaagaactt gtgtgtcccc caccctatcc cctctaacac 500  
cattcctcca cctgatgatg caactaacac ttgcctcccc actgcagcct 550  
goggctcctgc ccacctcccg tgatgtgtgt gtgtgtgtgt gtgtgtgact 600  
gtgtgtgttt gctaactgtg gtctttgtgg ctacttgttt gtggatggta 650  
ttgtgtttgt tagtgaactg tggactcgtt ttcccaggca ggggctgagc 700  
cacatggcca tctgtcctc cctgcccccg tggccctcca tcaccttctg 750  
ctcctaggag gctgcttggt gcccgagacc agccccctcc cctgatttag 800  
ggatgcgtag ggtaagagca cgggcagtgg tcttcagtcg tcttgggacc 850  
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cctttaacaa aaaccttgct tccttatccc acctgatccc agtctgaagg 950  
tctcttagca actggagata caaagcaagg agctggtgag cccagcgttg 1000  
acgtcaggca ggctatgccc ttccgtggtt aatttcttcc caggggcttc 1050  
cacgaggagt ccccatctgc cccgcccctt cacagagcgc ccggggattc 1100  
caggcccagg gcttctactc tgcccctggg gaatgtgtcc cctgcatatc 1150  
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cctgcttctg agacttcaat ctacagccca gctcatccag atgcagacta 1250  
cagtcctctg aattgggtct ctggcaggca atagttgaag gactcctgtt 1300  
ccgttggggc cagcacaccg ggatggatgg agggagagca gaggcctttg 1350  
cttctctgcc tacgtcccct tagatgggca gcagaggcaa ctcccgcatc 1400

ctttgctctg cctgtcgggtg gtcagagcgg tgagcgaggt gggttggaga 1450  
 ctcagcaggc tccgtgcagc ccttggaac agtgagaggt tgaaggtcat 1500  
 aacgagagtg ggaactcaac ccagatcccg cccctcctgt cctctgtgtt 1550  
 cccgcggaaa ccaaccaaac cgtgcgctgt gaccattgc tgttctctgt 1600  
 atcgtgatct atcctcaaca acaacagaaa aaaggaataa aatattcttt 1650  
 gtttcct 1657

<210> 199  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 199  
 Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met  
     1                    5                    10                    15  
 Val Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe  
                     20                    25                    30  
 His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala  
                     35                    40                    45  
 Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg  
                     50                    55                    60  
 Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu  
                     65                    70                    75  
 Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro  
                     80                    85                    90  
 Gln Lys Gln Arg Thr Glu Val Gln Pro Ser Gly Gly Ser Leu Trp  
                     95                    100                    105  
 Asn Leu Arg Arg Leu Leu Glu Pro Leu Asp Ala Asn Val Asp Ala  
                     110                    115                    120

<210> 200  
 <211> 415  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
 aaacttgacg ccatgaagat cccggtcctt cctgcggtgg tgctcctctc 50  
 cctcctgggtg ctccactctg cccagggagc caccctgggt ggtcctgagg 100  
 aagaaagcac cattgagaat tatgcgtcac gacccgaggc ctttaacacc 150  
 ccgttcctga acatcgacaa attgcgatct gcgtttaagg ctgatgagtt 200  
 cctgaactgg cacgccctct ttgagtctat caaaaggaaa cttcctttcc 250  
 tcaactggga tgcctttcct aagctgaaag gactgaggag cgcaactcct 300  
 gatgccagtg gaccatgacc tccactggaa gagggggcta gcgtgagcgc 350  
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cattttccat ccaaa 415

<210> 201

<211> 99

<212> PRT

<213> Homo sapiens

<400> 201

Met	Lys	Ile	Pro	Val	Leu	Pro	Ala	Val	Val	Leu	Leu	Ser	Leu	Leu
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Val	Leu	His	Ser	Ala	Gln	Gly	Ala	Thr	Leu	Gly	Gly	Pro	Glu	Glu
				20					25					30
Glu	Ser	Thr	Ile	Glu	Asn	Tyr	Ala	Ser	Arg	Pro	Glu	Ala	Phe	Asn
				35					40					45
Thr	Pro	Phe	Leu	Asn	Ile	Asp	Lys	Leu	Arg	Ser	Ala	Phe	Lys	Ala
				50					55					60
Asp	Glu	Phe	Leu	Asn	Trp	His	Ala	Leu	Phe	Glu	Ser	Ile	Lys	Arg
				65					70					75
Lys	Leu	Pro	Phe	Leu	Asn	Trp	Asp	Ala	Phe	Pro	Lys	Leu	Lys	Gly
				80					85					90
Leu	Arg	Ser	Ala	Thr	Pro	Asp	Ala	Gln						
				95										

<210> 202

<211> 678

<212> DNA

<213> Homo sapiens

<400> 202

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ggtggagatt gcctttgcct cagtgattct cacctgcctc tcccttctgg 100  
cagcaggagt ctcccaggtt gttcttctcc agccagttcc aactcaggag 150  
acagggtccca aggccatggg agatctctcc tgtggctttg ccggccactc 200  
atgagagtgt ttttgtgtaa agtatttttt agaatactgt tgacttcttc 250  
atgatttaat aaccatcctt tgcgaagttt tatgaggctt taggggaatg 300  
tcaaccctca aatttttggt atactagatg gcttccattt acccaccact 350  
attttaaggt ccctttattt ttaggttcaa ggttcatttg acttgagaaa 400  
gtgcccttct gcagcttcat tgattttggt tatcttctact attaatgtga 450  
acgattaaaa aagaataaga gcacgcagac ctctaggaga atattttatc 500  
cctgggtgcc cctgacacat ttatgtagtg atcccacaaa tgtgattggt 550  
aatttaaatg ttatttctaat attagtacat tcagttgtga tgtaatatga 600  
ataaccagaa tctatttctt aaaagttttg agtatatttt tcaactagat 650  
atttgatatg aaagactgaa tagtgatg 678

<210> 203  
<211> 52  
<212> PRT  
<213> Homo sapiens

<400> 203  
Met Gly Val Glu Ile Ala Phe Ala Ser Val Ile Leu Thr Cys Leu  
1 5 10 15  
Ser Leu Leu Ala Ala Gly Val Ser Gln Val Val Leu Leu Gln Pro  
20 25 30  
Val Pro Thr Gln Glu Thr Gly Pro Lys Ala Met Gly Asp Leu Ser  
35 40 45  
Cys Gly Phe Ala Gly His Ser  
50

<210> 204  
<211> 1917  
<212> DNA  
<213> Homo sapiens

<400> 204  
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gcttcggctc tggctgctgt tgttctcct gccctcagcg cagggccgcc 100  
agaaggagtc aggttcaaaa tggaaagtat ttattgacca aattaacagg 150  
tctttggaga attacgaacc atgttcaagt caaaactgca gctgctacca 200  
tggtgtcata gaagaggatc taactccttt ccgaggaggc atctccagga 250  
agatgatggc agaggtagtc agacggaagc tagggacca ctatcagatc 300  
actaagaaca gactgtaccg ggaaaatgac tgcattgtcc cctcaagggtg 350  
tagtggtggt gagcacttta ttttggaaagt gatcgggcgt ctccctgaca 400  
tggagatggt gatcaatgta cgagattatc ctgaggttcc taaatggatg 450  
gagcctgcca tcccagtctt ctcttcagt aagacatcag agtaccatga 500  
tatcatgtat cctgcttggc cattttggga agggggacct gctgtttggc 550  
caatttatcc tacaggtctt ggacggtggg acctcttcag agaagatctg 600  
gtaagggtcag cagcacagtg gccatggaaa aagaaaaact ctacagcata 650  
tttccgagga tcaaggacaa gtccagaacg agatcctctc attcttctgt 700  
ctcggaaaaa cccaaaactt gttgatgcag aatacaccaa aaaccaggcc 750  
tggaaatcta tgaaagatac cttaggaaaag ccagctgcta aggatgtcca 800  
tcttgtggat cactgcaaat acaagtatct gtttaatttt cgaggcgtag 850  
ctgcaagttt ccggtttaa cacctcttcc tgtgtggctc acttgttttc 900  
catgttggtg atgagtggct agaattcttc tatccacagc tgaagccatg 950  
ggttcactat atcccagtca aaacagatct ctccaatgtc caagagctgt 1000

tacaatttgt aaaagcaa at gatgatgtag ctcaagagat tgctgaaagg 1050  
 ggaagccagt ttattaggaa ccatttgcag atggatgaca tcacctgtta 1100  
 ctgggagaac ctcttgagtg aatactctaa attcctgtct tataatgtaa 1150  
 cgagaaggaa aggttatgat caaattattc ccaaaatgtt gaaaactgaa 1200  
 ctatagtagt catcatagga ccatagtcct ctttgtggca acagatctca 1250  
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 agttcaactt tttggatgaa taaggaccag aaatcgtgag atgtggattt 1450  
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 tcagatcatc cacctgtgtg agtccatcac tgtgaaattg actgtgtcca 1550  
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 gaagtagtac aactcattgc tggaattgtg aaattattca aggcgtgatc 1650  
 tctgtcactt tattttaatg taggaaacc tatgggggtt atgaaaaata 1700  
 cttggggatc attctctgaa tgggtctaagg aagcggtagc catgccatgc 1750  
 aatgatgtag gagttctctt ttgtaaaacc ataaactctg ttactcagga 1800  
 ggtttctata atgccacata gaaagaggcc aattgcatga gtaattattg 1850  
 caattggatt tcagggtccc ttttctgtgcc ttcatgccct actttottaat 1900  
 gcctctctaa agccaaa 1917

<210> 205  
 <211> 392  
 <212> PRT  
 <213> Homo sapiens

<400> 205  
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 Phe Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser  
 20 25 30  
 Lys Trp Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn  
 35 40 45  
 Tyr Glu Pro Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val  
 50 55 60  
 Ile Glu Glu Asp Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys  
 65 70 75  
 Met Met Ala Glu Val Val Arg Arg Lys Leu Gly Thr His Tyr Gln  
 80 85 90  
 Ile Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro

	95	100	105
Ser Arg Cys Ser Gly Val Glu His Phe Ile Leu Glu Val Ile Gly	110	115	120
Arg Leu Pro Asp Met Glu Met Val Ile Asn Val Arg Asp Tyr Pro	125	130	135
Gln Val Pro Lys Trp Met Glu Pro Ala Ile Pro Val Phe Ser Phe	140	145	150
Ser Lys Thr Ser Glu Tyr His Asp Ile Met Tyr Pro Ala Trp Thr	155	160	165
Phe Trp Glu Gly Gly Pro Ala Val Trp Pro Ile Tyr Pro Thr Gly	170	175	180
Leu Gly Arg Trp Asp Leu Phe Arg Glu Asp Leu Val Arg Ser Ala	185	190	195
Ala Gln Trp Pro Trp Lys Lys Lys Asn Ser Thr Ala Tyr Phe Arg	200	205	210
Gly Ser Arg Thr Ser Pro Glu Arg Asp Pro Leu Ile Leu Leu Ser	215	220	225
Arg Lys Asn Pro Lys Leu Val Asp Ala Glu Tyr Thr Lys Asn Gln	230	235	240
Ala Trp Lys Ser Met Lys Asp Thr Leu Gly Lys Pro Ala Ala Lys	245	250	255
Asp Val His Leu Val Asp His Cys Lys Tyr Lys Tyr Leu Phe Asn	260	265	270
Phe Arg Gly Val Ala Ala Ser Phe Arg Phe Lys His Leu Phe Leu	275	280	285
Cys Gly Ser Leu Val Phe His Val Gly Asp Glu Trp Leu Glu Phe	290	295	300
Phe Tyr Pro Gln Leu Lys Pro Trp Val His Tyr Ile Pro Val Lys	305	310	315
Thr Asp Leu Ser Asn Val Gln Glu Leu Leu Gln Phe Val Lys Ala	320	325	330
Asn Asp Asp Val Ala Gln Glu Ile Ala Glu Arg Gly Ser Gln Phe	335	340	345
Ile Arg Asn His Leu Gln Met Asp Asp Ile Thr Cys Tyr Trp Glu	350	355	360
Asn Leu Leu Ser Glu Tyr Ser Lys Phe Leu Ser Tyr Asn Val Thr	365	370	375
Arg Arg Lys Gly Tyr Asp Gln Ile Ile Pro Lys Met Leu Lys Thr	380	385	390
Glu Leu			

<210> 206

<211> 1425  
<212> DNA  
<213> Homo sapiens

<400> 206  
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ccctcgctc tttcatcctg gcctttggca ccggagtga gttcgtgogc 100  
tttacctccc ttcgccact tcttgaggg atcccgagt ctggtggtcc 150  
ggatgccgc cagggatggc tggctgccct gcaggaccgc agcatccttg 200  
ccccctggc atgggatctg gggctcctgc ttctatattgt tgggcagcac 250  
agcctcatgg cagctgaaag agtgaaggca tggacatccc ggtactttgg 300  
ggtccttcag aggtcactgt atgtggcctg cactgccctg gccttgcagc 350  
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gctcgggctg agccatgggc cacctgggtg ccgctcctct gctttgtgct 450  
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atgctgagct catgggcctc aaacaggat actaccatgt gotggggctg 550  
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ccagctacaa agaaaactcc acctgctctc tgggcccag gatggggagg 800  
cagagtgagg agctcactct ggttacaagc cctgttcttc ctctccact 850  
gaattctaaa tccttaacat ccaggccctg gctgcttcat gccagaggcc 900  
caaatccatg gactgaagga gatgcccctt ctactacttg agactttatt 950  
ctctgggtcc agctccatac cctaaattct gagtttcagc cactgaactc 1000  
caaggtccac ttctcaccag caaggaagag tggggtatgg aagtcactg 1050  
tcccttact gtttagagca tgacactctc cccctcaaca gcctcctgag 1100  
aaggaaagga tctgcctga ccaactcccct ggcactgtta cttgcctctg 1150  
cgctcaggg gtccccctt gcaccgctg cttccactcc aagaagggtg 1200  
accagggctt gcaagttcaa cggtcatagc tgtccctcca ggccccaacc 1250  
ttgcctcacc actcccggc ctagtctctg cacctcctta ggccctgcct 1300  
ctgggctcag accccaacct agtcaagggg attctcctgc tottaactcg 1350  
atgacttggg gctccctgct ctcccagga agatgctctg caggaaaata 1400  
aaagtcagcc tttttctaaa aaaaa 1425

<210> 207  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<400> 207

Met	Ala	Pro	Ala	Leu	Leu	Leu	Ile	Pro	Ala	Ala	Leu	Ala	Ser	Phe
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Ile	Leu	Ala	Phe	Gly	Thr	Gly	Val	Glu	Phe	Val	Arg	Phe	Thr	Ser
				20					25					30
Leu	Arg	Pro	Leu	Leu	Gly	Gly	Ile	Pro	Glu	Ser	Gly	Gly	Pro	Asp
				35					40					45
Ala	Arg	Gln	Gly	Trp	Leu	Ala	Ala	Leu	Gln	Asp	Arg	Ser	Ile	Leu
				50					55					60
Ala	Pro	Leu	Ala	Trp	Asp	Leu	Gly	Leu	Leu	Leu	Leu	Phe	Val	Gly
				65					70					75
Gln	His	Ser	Leu	Met	Ala	Ala	Glu	Arg	Val	Lys	Ala	Trp	Thr	Ser
				80					85					90
Arg	Tyr	Phe	Gly	Val	Leu	Gln	Arg	Ser	Leu	Tyr	Val	Ala	Cys	Thr
				95					100					105
Ala	Leu	Ala	Leu	Gln	Leu	Val	Met	Arg	Tyr	Trp	Glu	Pro	Ile	Pro
				110					115					120
Lys	Gly	Pro	Val	Leu	Trp	Glu	Ala	Arg	Ala	Glu	Pro	Trp	Ala	Thr
				125					130					135
Trp	Val	Pro	Leu	Leu	Cys	Phe	Val	Leu	His	Val	Ile	Ser	Trp	Leu
				140					145					150
Leu	Ile	Phe	Ser	Ile	Leu	Leu	Val	Phe	Asp	Tyr	Ala	Glu	Leu	Met
				155					160					165
Gly	Leu	Lys	Gln	Val	Tyr	Tyr	His	Val	Leu	Gly	Leu	Gly	Glu	Pro
				170					175					180
Leu	Ala	Leu	Lys	Ser	Pro	Arg	Ala	Leu	Arg	Leu	Phe	Ser	His	Leu
				185					190					195
Arg	His	Pro	Val	Cys	Val	Glu	Leu	Leu	Thr	Val	Leu	Trp	Val	Val
				200					205					210
Pro	Thr	Leu	Gly	Thr	Asp	Arg	Leu	Leu	Leu	Ala	Phe	Leu	Leu	Thr
				215					220					225
Leu	Tyr	Leu	Gly	Leu	Ala	His	Gly	Leu	Asp	Gln	Gln	Asp	Leu	Arg
				230					235					240
Tyr	Leu	Arg	Ala	Gln	Leu	Gln	Arg	Lys	Leu	His	Leu	Leu	Ser	Arg
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Pro	Gln	Asp	Gly	Glu	Ala	Glu								
				260										

<210> 208  
 <211> 2095  
 <212> DNA

<213> Homo sapiens

<400> 208

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caacaaaaaa cttaagcttt aatttcatct ggaattccac agttttctta 200  
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cgtgcttctg agctgctgtg gatggcctcg gctctctgga ctgtccttcc 350  
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 caagataaaa aggatagtga atcattcttt acatgcaaac attttccagt 1950  
 tacttaactg atcagtttat tattgataca tcactccatt aatgtaaagt 2000  
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<210> 209

<211> 331

<212> PRT

<213> Homo sapiens

<400> 209

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			20					25						30
Phe	Val	Met	Trp	Tyr	Leu	Ser	Leu	Pro	His	Tyr	Asn	Val	Ile	Glu
			35					40						45
Arg	Val	Asn	Trp	Met	Tyr	Phe	Tyr	Glu	Tyr	Glu	Pro	Ile	Tyr	Arg
			50					55						60
Gln	Asp	Phe	His	Phe	Thr	Leu	Arg	Glu	His	Ser	Asn	Cys	Ser	His
			65					70						75
Gln	Asn	Pro	Phe	Leu	Val	Ile	Leu	Val	Thr	Ser	His	Pro	Ser	Asp
			80					85						90
Val	Lys	Ala	Arg	Gln	Ala	Ile	Arg	Val	Thr	Trp	Gly	Glu	Lys	Lys
			95					100						105
Ser	Trp	Trp	Gly	Tyr	Glu	Val	Leu	Thr	Phe	Phe	Leu	Leu	Gly	Gln
			110					115						120
Glu	Ala	Glu	Lys	Glu	Asp	Lys	Met	Leu	Ala	Leu	Ser	Leu	Glu	Asp
			125					130						135
Glu	His	Leu	Leu	Tyr	Gly	Asp	Ile	Ile	Arg	Gln	Asp	Phe	Leu	Asp
			140					145						150
Thr	Tyr	Asn	Asn	Leu	Thr	Leu	Lys	Thr	Ile	Met	Ala	Phe	Arg	Trp
			155					160						165

Val	Thr	Glu	Phe	Cys	Pro	Asn	Ala	Lys	Tyr	Val	Met	Lys	Thr	Asp	
				170					175					180	
Thr	Asp	Val	Phe	Ile	Asn	Thr	Gly	Asn	Leu	Val	Lys	Tyr	Leu	Leu	
				185					190					195	
Asn	Leu	Asn	His	Ser	Glu	Lys	Phe	Phe	Thr	Gly	Tyr	Pro	Leu	Ile	
				200					205					210	
Asp	Asn	Tyr	Ser	Tyr	Arg	Gly	Phe	Tyr	Gln	Lys	Thr	His	Ile	Ser	
				215					220					225	
Tyr	Gln	Glu	Tyr	Pro	Phe	Lys	Val	Phe	Pro	Pro	Tyr	Cys	Ser	Gly	
				230					235					240	
Leu	Gly	Tyr	Ile	Met	Ser	Arg	Asp	Leu	Val	Pro	Arg	Ile	Tyr	Glu	
				245					250					255	
Met	Met	Gly	His	Val	Lys	Pro	Ile	Lys	Phe	Glu	Asp	Val	Tyr	Val	
				260					265					270	
Gly	Ile	Cys	Leu	Asn	Leu	Leu	Lys	Val	Asn	Ile	His	Ile	Pro	Glu	
				275					280					285	
Asp	Thr	Asn	Leu	Phe	Phe	Leu	Tyr	Arg	Ile	His	Leu	Asp	Val	Cys	
				290					295					300	
Gln	Leu	Arg	Arg	Val	Ile	Ala	Ala	His	Gly	Phe	Ser	Ser	Lys	Glu	
				305					310					315	
Ile	Ile	Thr	Phe	Trp	Gln	Val	Met	Leu	Arg	Asn	Thr	Thr	Cys	His	
				320					325					330	

Tyr

<210> 210

<211> 745

<212> DNA

<213> Homo sapiens

<400> 210

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gtgtcaacaa tgaacacaat gtggccaatg ttgacaataa caacggatgg 200
gactcctgga attccatctg ggattatgga aatggctttg ctgcaaccag 250
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<211> 185  
<212> PRT  
<213> Homo sapiens

<400> 211  
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Asn Asn Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu  
35 40 45  
His Asn Val Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp  
50 55 60  
Asn Ser Ile Trp Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu  
65 70 75  
Phe Gln Lys Lys Thr Cys Ile Val His Lys Met Asn Lys Glu Val  
80 85 90  
Met Pro Ser Ile Gln Ser Leu Asp Ala Leu Val Lys Glu Lys Lys  
95 100 105  
Leu Gln Gly Lys Gly Pro Gly Gly Pro Pro Pro Lys Gly Leu Met  
110 115 120  
Tyr Ser Val Asn Pro Asn Lys Val Asp Asp Leu Ser Lys Phe Gly  
125 130 135  
Lys Asn Ile Ala Asn Met Cys Arg Gly Ile Pro Thr Tyr Met Ala  
140 145 150  
Glu Glu Met Gln Glu Ala Ser Leu Phe Phe Tyr Ser Gly Thr Cys  
155 160 165  
Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile Ser Phe Cys Gly  
170 175 180  
Asp Thr Val Glu Asn  
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<210> 212  
<211> 1706  
<212> DNA  
<213> Homo sapiens

<400> 212  
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 ttatatgcta gaatatgagg atgtgaatat aaataagaga agaaaaaaga 250  
 ataaagtaga ttgagtctcc aattttatgt aagcttcaga agaactgggtt 300  
 tgtttacatg caagcttata gttgaaatat ttttcaggaa ttacatgaat 350  
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 aagaacctga ggatagacaa caggcttcca aaagccctta caatggtgta 800  
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<210> 213

<211> 299

<212> PRT

<213> Homo sapiens

<400> 213

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Glu	Thr	Ile	Ala	Cys	Ala	Cys	Ile	Tyr	Leu	Ala	Ala	Arg	Ala	Leu	
				20					25					30	
Gln	Ile	Pro	Leu	Pro	Thr	Arg	Pro	His	Trp	Phe	Leu	Leu	Phe	Gly	
				35					40					45	
Thr	Thr	Glu	Glu	Glu	Ile	Gln	Glu	Ile	Cys	Ile	Glu	Thr	Leu	Arg	
				50					55					60	
Leu	Tyr	Thr	Arg	Lys	Lys	Pro	Asn	Tyr	Glu	Leu	Leu	Glu	Lys	Glu	
				65					70					75	
Val	Glu	Lys	Arg	Lys	Val	Ala	Leu	Gln	Glu	Ala	Lys	Leu	Lys	Ala	
				80					85					90	
Lys	Gly	Leu	Asn	Pro	Asp	Gly	Thr	Pro	Ala	Leu	Ser	Thr	Leu	Gly	
				95					100					105	
Gly	Phe	Ser	Pro	Ala	Ser	Lys	Pro	Ser	Ser	Pro	Arg	Glu	Val	Lys	
				110					115					120	
Ala	Glu	Glu	Lys	Ser	Pro	Ile	Ser	Ile	Asn	Val	Lys	Thr	Val	Lys	
				125					130					135	
Lys	Glu	Pro	Glu	Asp	Arg	Gln	Gln	Ala	Ser	Lys	Ser	Pro	Tyr	Asn	
				140					145					150	
Gly	Val	Arg	Lys	Asp	Ser	Lys	Arg	Ser	Arg	Asn	Ser	Arg	Ser	Ala	
				155					160					165	
Ser	Arg	Ser	Arg	Ser	Arg	Thr	Arg	Ser	Arg	Ser	Arg	Ser	His	Thr	
				170					175					180	
Pro	Arg	Arg	His	Tyr	Asn	Asn	Arg	Arg	Ser	Arg	Ser	Gly	Thr	Tyr	
				185					190					195	
Ser	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	His	Ser	Glu	Ser	Pro	
				200					205					210	
Arg	Arg	His	His	Asn	His	Gly	Ser	Pro	His	Leu	Lys	Ala	Lys	His	
				215					220					225	
Thr	Arg	Asp	Asp	Leu	Lys	Ser	Ser	Asn	Arg	His	Gly	His	Lys	Arg	
				230					235					240	
Lys	Lys	Ser	Arg	Ser	Arg	Ser	Gln	Ser	Lys	Ser	Arg	Asp	His	Ser	
				245					250					255	
Asp	Ala	Ala	Lys	Lys	His	Arg	His	Glu	Arg	Gly	His	His	Arg	Asp	
				260					265					270	
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<210> 214

<211> 730

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 72-73, 85, 91, 127, 226, 268, 454, 484, 513, 566, 663

<223> unknown base

<400> 214

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ggattgtaat atgaaattat ttaaaagggc ttcgctcata tataggaaaa 200  
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agccaaacta tgaattactg gaaaaagaag tagaaaaaag aaaagtagcc 650  
ttacaagaag ccnaattaaa agcaaaggga ttgaatcogg atggaactcc 700  
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<210> 215

<211> 1807

<212> DNA

<213> Homo sapiens

<400> 215

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ccaccctcat gcacaggctg gcgccacact gctccttcgc gcgctggctg 150  
ctctgtaacg gcagtttgtt ccgatacaag caccctgtctg aggaggagct 200  
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<210> 216

<211> 479  
 <212> PRT  
 <213> Homo sapiens

<400> 216

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				20					25					30	
Leu	Leu	Cys	Asn	Gly	Ser	Leu	Phe	Arg	Tyr	Lys	His	Pro	Ser	Glu	
				35					40					45	
Glu	Glu	Leu	Arg	Ala	Leu	Ala	Gly	Lys	Pro	Arg	Pro	Arg	Gly	Arg	
				50					55					60	
Lys	Glu	Arg	Trp	Ala	Asn	Gly	Leu	Ser	Glu	Glu	Lys	Pro	Leu	Ser	
				65					70					75	
Val	Pro	Arg	Asp	Ala	Pro	Phe	Gln	Leu	Glu	Thr	Cys	Pro	Leu	Thr	
				80					85					90	
Thr	Val	Asp	Ala	Leu	Val	Leu	Arg	Phe	Phe	Leu	Glu	Tyr	Gln	Trp	
				95					100					105	
Phe	Val	Asp	Phe	Ala	Val	Tyr	Ser	Gly	Gly	Val	Tyr	Leu	Phe	Thr	
				110					115					120	
Glu	Ala	Tyr	Tyr	Tyr	Met	Leu	Gly	Pro	Ala	Lys	Glu	Thr	Asn	Ile	
				125					130					135	
Ala	Val	Phe	Trp	Cys	Leu	Leu	Thr	Val	Thr	Phe	Ser	Ile	Lys	Met	
				140					145					150	
Phe	Leu	Thr	Val	Thr	Arg	Leu	Tyr	Phe	Ser	Ala	Glu	Glu	Gly	Gly	
				155					160					165	
Glu	Arg	Ser	Val	Cys	Leu	Thr	Phe	Ala	Phe	Leu	Phe	Leu	Leu	Leu	
				170					175					180	
Ala	Met	Leu	Val	Gln	Val	Val	Arg	Glu	Glu	Thr	Leu	Glu	Leu	Gly	
				185					190					195	
Leu	Glu	Pro	Gly	Leu	Ala	Ser	Met	Thr	Gln	Asn	Leu	Glu	Pro	Leu	
				200					205					210	
Leu	Lys	Lys	Gln	Gly	Trp	Asp	Trp	Ala	Leu	Pro	Val	Ala	Lys	Leu	
				215					220					225	
Ala	Ile	Arg	Val	Gly	Leu	Ala	Val	Val	Gly	Ser	Val	Leu	Gly	Ala	
				230					235					240	
Phe	Leu	Thr	Phe	Pro	Gly	Leu	Arg	Leu	Ala	Gln	Thr	His	Arg	Asp	
				245					250					255	
Ala	Leu	Thr	Met	Ser	Glu	Asp	Arg	Pro	Met	Leu	Gln	Phe	Leu	Leu	
				260					265					270	
His	Thr	Ser	Phe	Leu	Ser	Pro	Leu	Phe	Ile	Leu	Trp	Leu	Trp	Thr	
				275					280					285	
Lys	Pro	Ile	Ala	Arg	Asp	Phe	Leu	His	Gln	Pro	Pro	Phe	Gly	Glu	

290					295					300				
Thr	Arg	Phe	Ser	Leu	Leu	Ser	Asp	Ser	Ala	Phe	Asp	Ser	Gly	Arg
				305					310					315
Leu	Trp	Leu	Leu	Val	Val	Leu	Cys	Leu	Leu	Arg	Leu	Ala	Val	Thr
				320					325					330
Arg	Pro	His	Leu	Gln	Ala	Tyr	Leu	Cys	Leu	Ala	Lys	Ala	Arg	Val
				335					340					345
Glu	Gln	Leu	Arg	Arg	Glu	Ala	Gly	Arg	Ile	Glu	Ala	Arg	Glu	Ile
				350					355					360
Gln	Gln	Arg	Val	Val	Arg	Val	Tyr	Cys	Tyr	Val	Thr	Val	Val	Ser
				365					370					375
Leu	Gln	Tyr	Leu	Thr	Pro	Leu	Ile	Leu	Thr	Leu	Asn	Cys	Thr	Leu
				380					385					390
Leu	Leu	Lys	Thr	Leu	Gly	Gly	Tyr	Ser	Trp	Gly	Leu	Gly	Pro	Ala
				395					400					405
Pro	Leu	Leu	Ser	Pro	Asp	Pro	Ser	Ser	Ala	Ser	Ala	Ala	Pro	Ile
				410					415					420
Gly	Ser	Gly	Glu	Asp	Glu	Val	Gln	Gln	Thr	Ala	Ala	Arg	Ile	Ala
				425					430					435
Gly	Ala	Leu	Gly	Gly	Leu	Leu	Thr	Pro	Leu	Phe	Leu	Arg	Gly	Val
				440					445					450
Leu	Ala	Tyr	Leu	Ile	Trp	Trp	Thr	Ala	Ala	Cys	Gln	Leu	Leu	Ala
				455					460					465
Ser	Leu	Phe	Gly	Leu	Tyr	Phe	His	Gln	His	Leu	Ala	Gly	Ser	
				470					475					

<210> 217  
 <211> 574  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 5, 146  
 <223> unknown base

<400> 217  
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 gctcactgcc accctcatgc acaggctggc gccacactgc tccttcgcgc 100  
 gctggctgct ctgtaacggc agtttggtcc gatacaagca cccgtnttga 150  
 ggaggagctt cgggccctgg cggggaagcc gagggccaga ggcaggaaag 200  
 agcgggtgggc caatggcctt agtgaggaga agccactgtc tgtgccccga 250  
 gatgccccgt tccagctgga gacctgcccc ctcacgaccg tggatgccct 300  
 ggtcctgcgc ttcttcctgg agtaccagtg gtttgtggac tttgctgtgt 350

actcggggcgg cgtgtacctc ttcacagagg cctactacta catgctggga 400  
ccagccaagg agactaacat tgctgtgttc tggcgctgc tcacagtgc 450  
cttctccatc aagatgttcc tgacagtgc acggctgtac ttcagcgccg 500  
aggagggggg tgagcgctct gtctgcctca cctttgcctt cctcttctg 550  
ctgctggcca tgctggtgca agcg 574

<210> 218  
<211> 2571  
<212> DNA  
<213> Homo sapiens

<400> 218  
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ttgtgatcta ctgattgtgg gggcatggca aggtttgctt aaaggagctt 150  
ggctgggttg ggcccttgta gctgacagaa ggtggccagg gagaatgcag 200  
cacactgctc ggagaatgaa ggcgcttctg ttgctggtct tgccttggct 250  
cagtcctgct aactacattg acaatgtggg caacctgcac ttctgtatt 300  
cagaactctg taaaggtgcc tcccactacg gcctgaccaa agataggaag 350  
aggcgctcac aagatggctg tccagacggc tgtgcgagcc tcacagccac 400  
ggctccctcc ccagagggtt ctgcagctgc caccatctcc ttaatgacag 450  
acgagcctgg cctagacaac cctgcctacg tgtcctcggc agaggacggg 500  
cagccagcaa tcagcccagt ggactctggc cggagcaacc gaactagggc 550  
acggcccttt gagagatcca ctattagaag cagatcattt aaaaaataa 600  
atcgagcttt gagtgttctt cgaaggacaa agagcgggag tgcagttgcc 650  
aaccatgccg accagggcag ggaaaattct gaaaacacca ctgcccctga 700  
agtctttcca aggttgtacc acctgattcc agatggtgaa attaccagca 750  
tcaagatcaa tcgagtagat ccagtgaaa gcctctctat taggctggtg 800  
ggaggtagcg aaaccccact ggtccatata attatccaac acatttatcg 850  
tgatggggtg atcgccagag acggccggct actgccagga gacatcattc 900  
taaaggatcaa cgggatggac atcagcaatg tccctcacia ctacgctgtg 950  
cgtctctctgc ggcagccctg ccaggtgctg tggctgactg tgatgcgtga 1000  
acagaagtgc cgcagcagga acaatggaca ggccccggat gcctacagac 1050  
cccgagatga cagctttcat gtgattctca acaaaagtag ccccgaggag 1100  
cagcttggaa taaaactggt gcgcaagggt gatgagcctg gggttttcat 1150  
cttcaatgtg ctggatggcg gtgtggcata tcgacatggt cagcttgagg 1200

agaatgaccg tgtgttagcc atcaatggac atgatcttcg atatggcagc 1250  
 ccagaaagtg cggctcatct gattcaggcc agtgaaagac gtgttcacct 1300  
 cgtcgtgtcc cgccagggtc ggccagcggag ccctgacatc tttcaggaag 1350  
 ccggctggaa cagcaatggc agctgggtccc cagggccagg ggagaggagc 1400  
 aacactccca agcccctcca tcctacaatt acttgtcatg agaaggtggt 1450  
 aaatatccaa aaagaccccc gtgaatctct cggcatgacc gtcgcagggg 1500  
 gagcatcaca tagagaatgg gatttgccta tctatgtcat cagtgttgag 1550  
 cccggaggag tcataagcag agatggaaga ataaaaacag gtgacatttt 1600  
 gttgaatgtg gatgggggtc aactgacaga ggtcagccgg agtgaggcag 1650  
 tggcattatt gaaaagaaca tcctcctoga tagtactcaa agctttggaa 1700  
 gtcaaagagt atgagcccca ggaagactgc agcagcccag cagccctgga 1750  
 ctccaaccac aacatggccc caccagtgga ctgggtccca tcctgggtca 1800  
 tgtggctgga attaccacgg tgcttgtata actgtaaaga tattgtatta 1850  
 cgaagaaaca cagctggaag tctgggcttc tgcattgtag gaggttatga 1900  
 agaatacaat ggaaacaaac cttttttcat caaatccatt gttgaaggaa 1950  
 caccagcata caatgatgga agaattagat gtggtgatat tcttcttgct 2000  
 gtcaatggta gaagtacatc aggaatgata catgcttgct tggcaagact 2050  
 gctgaaagaa cttaaaggaa gaattactct aactattgtt tcttggcctg 2100  
 gcactttttt atagaatcaa tgatgggtca gaggaaaaca gaaaaatcac 2150  
 aaataggcta agaagttgaa aactatatt tatcttgtca gttttatat 2200  
 ttaaagaaag aatacattgt aaaaatgtca ggaaaagtat gatcatctaa 2250  
 tgaaagccag ttacacctca gaaaatatga ttccaaaaaa attaaaacta 2300  
 ctagtttttt ttcagtgtgg aggatttctc attactctac aacattgttt 2350  
 atattttttt tattcaataa aaagccctaa aacaactaaa atgattgatt 2400  
 tgtatacccc actgaattca agctgattta aatttaaaat ttggtatatg 2450  
 ctgaagtctg ccaagggtag attatggcca tttttaattt acagctaaaa 2500  
 tattttttta aatgcattgc tgagaaacgt tgctttcatc aaacaagaat 2550  
 aaatattttt cagaagttaa a 2571

<210> 219

<211> 632

<212> PRT

<213> Homo sapiens

<400> 219

Met Lys Ala Leu Leu Leu Leu Val Leu Pro Trp Leu Ser Pro Ala

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Asn Tyr Ile Asp	Asn Val Gly Asn Leu His Phe Leu Tyr Ser Glu		
	20	25	30
Leu Cys Lys Gly	Ala Ser His Tyr Gly Leu Thr Lys Asp Arg Lys		
	35	40	45
Arg Arg Ser Gln Asp	Gly Cys Pro Asp Gly Cys Ala Ser Leu Thr		
	50	55	60
Ala Thr Ala Pro Ser	Pro Glu Val Ser Ala Ala Ala Thr Ile Ser		
	65	70	75
Leu Met Thr Asp	Glu Pro Gly Leu Asp Asn Pro Ala Tyr Val Ser		
	80	85	90
Ser Ala Glu Asp	Gly Gln Pro Ala Ile Ser Pro Val Asp Ser Gly		
	95	100	105
Arg Ser Asn Arg	Thr Arg Ala Arg Pro Phe Glu Arg Ser Thr Ile		
	110	115	120
Arg Ser Arg Ser	Phe Lys Lys Ile Asn Arg Ala Leu Ser Val Leu		
	125	130	135
Arg Arg Thr Lys	Ser Gly Ser Ala Val Ala Asn His Ala Asp Gln		
	140	145	150
Gly Arg Glu Asn	Ser Glu Asn Thr Thr Ala Pro Glu Val Phe Pro		
	155	160	165
Arg Leu Tyr His	Leu Ile Pro Asp Gly Glu Ile Thr Ser Ile Lys		
	170	175	180
Ile Asn Arg Val	Asp Pro Ser Glu Ser Leu Ser Ile Arg Leu Val		
	185	190	195
Gly Gly Ser Glu	Thr Pro Leu Val His Ile Ile Ile Gln His Ile		
	200	205	210
Tyr Arg Asp Gly	Val Ile Ala Arg Asp Gly Arg Leu Leu Pro Gly		
	215	220	225
Asp Ile Ile Leu	Lys Val Asn Gly Met Asp Ile Ser Asn Val Pro		
	230	235	240
His Asn Tyr Ala	Val Arg Leu Leu Arg Gln Pro Cys Gln Val Leu		
	245	250	255
Trp Leu Thr Val	Met Arg Glu Gln Lys Phe Arg Ser Arg Asn Asn		
	260	265	270
Gly Gln Ala Pro	Asp Ala Tyr Arg Pro Arg Asp Asp Ser Phe His		
	275	280	285
Val Ile Leu Asn	Lys Ser Ser Pro Glu Glu Gln Leu Gly Ile Lys		
	290	295	300
Leu Val Arg Lys	Val Asp Glu Pro Gly Val Phe Ile Phe Asn Val		
	305	310	315
Leu Asp Gly Gly	Val Ala Tyr Arg His Gly Gln Leu Glu Glu Asn		

320										325					330				
Asp	Arg	Val	Leu	Ala	Ile	Asn	Gly	His	Asp	Leu	Arg	Tyr	Gly	Ser					
				335					340					345					
Pro	Glu	Ser	Ala	Ala	His	Leu	Ile	Gln	Ala	Ser	Glu	Arg	Arg	Val					
				350					355					360					
His	Leu	Val	Val	Ser	Arg	Gln	Val	Arg	Gln	Arg	Ser	Pro	Asp	Ile					
				365					370					375					
Phe	Gln	Glu	Ala	Gly	Trp	Asn	Ser	Asn	Gly	Ser	Trp	Ser	Pro	Gly					
				380					385					390					
Pro	Gly	Glu	Arg	Ser	Asn	Thr	Pro	Lys	Pro	Leu	His	Pro	Thr	Ile					
				395					400					405					
Thr	Cys	His	Glu	Lys	Val	Val	Asn	Ile	Gln	Lys	Asp	Pro	Gly	Glu					
				410					415					420					
Ser	Leu	Gly	Met	Thr	Val	Ala	Gly	Gly	Ala	Ser	His	Arg	Glu	Trp					
				425					430					435					
Asp	Leu	Pro	Ile	Tyr	Val	Ile	Ser	Val	Glu	Pro	Gly	Gly	Val	Ile					
				440					445					450					
Ser	Arg	Asp	Gly	Arg	Ile	Lys	Thr	Gly	Asp	Ile	Leu	Leu	Asn	Val					
				455					460					465					
Asp	Gly	Val	Glu	Leu	Thr	Glu	Val	Ser	Arg	Ser	Glu	Ala	Val	Ala					
				470					475					480					
Leu	Leu	Lys	Arg	Thr	Ser	Ser	Ser	Ile	Val	Leu	Lys	Ala	Leu	Glu					
				485					490					495					
Val	Lys	Glu	Tyr	Glu	Pro	Gln	Glu	Asp	Cys	Ser	Ser	Pro	Ala	Ala					
				500					505					510					
Leu	Asp	Ser	Asn	His	Asn	Met	Ala	Pro	Pro	Ser	Asp	Trp	Ser	Pro					
				515					520					525					
Ser	Trp	Val	Met	Trp	Leu	Glu	Leu	Pro	Arg	Cys	Leu	Tyr	Asn	Cys					
				530					535					540					
Lys	Asp	Ile	Val	Leu	Arg	Arg	Asn	Thr	Ala	Gly	Ser	Leu	Gly	Phe					
				545					550					555					
Cys	Ile	Val	Gly	Gly	Tyr	Glu	Glu	Tyr	Asn	Gly	Asn	Lys	Pro	Phe					
				560					565					570					
Phe	Ile	Lys	Ser	Ile	Val	Glu	Gly	Thr	Pro	Ala	Tyr	Asn	Asp	Gly					
				575					580					585					
Arg	Ile	Arg	Cys	Gly	Asp	Ile	Leu	Leu	Ala	Val	Asn	Gly	Arg	Ser					
				590					595					600					
Thr	Ser	Gly	Met	Ile	His	Ala	Cys	Leu	Ala	Arg	Leu	Leu	Lys	Glu					
				605					610					615					
Leu	Lys	Gly	Arg	Ile	Thr	Leu	Thr	Ile	Val	Ser	Trp	Pro	Gly	Thr					
				620					625					630					

Phe Leu

<210> 220  
<211> 773  
<212> DNA  
<213> Homo sapiens

<400> 220  
ccaaagtgat catttgaaaa agagatatcc acatcttcaa gcccatataa 50  
aggatagaag ctgcacaggg cagctttact tactccagca ccttcctctc 100  
ccaggcaaat ggtgctgacc atctttggga tacaatctca tggatacgag 150  
gtttttaaca tcacagccc aagcaacaat ggtggcaatg ttcaggagac 200  
agtgacaatt gataatgaaa aaaataccgc catcgттаac atccatgcag 250  
gatcatgctc ttctaccaca atttttgact ataaacatgg ctacattgca 300  
tccaggggtgc tctccgaag agcctgcttt atcctgaaga tggaccatca 350  
gaacatccct cctctgaaca atctccaatg gtacatctat gagaaacagg 400  
ctctggacaa catgttctcc aacaaatata cctgggtcaa gtacaaccct 450  
ctggagtctc tgatcaaaga cgtggattgg ttctgcttg ggtcacccat 500  
tgagaaactc tgcaaacata tccctttgta taagggggaa gtggttgaaa 550  
acacacataa tgtcgggtgct ggaggctgtg caaaggctgg gctcctgggc 600  
atcttgggaa tttcaatctg tgcagacatt catgtttagg atgattagcc 650  
ctcttgtttt atcttttcaa agaaatacat ccttggttta cactcaaaag 700  
tcaaattaaa ttctttccca atgccccaac taattttgag attcagtcag 750  
aaaatataaa tgctgtattt ata 773

<210> 221  
<211> 184  
<212> PRT  
<213> Homo sapiens

<400> 221  
Met Lys Ile Leu Val Ala Phe Leu Val Val Leu Thr Ile Phe Gly  
1 5 10 15  
Ile Gln Ser His Gly Tyr Glu Val Phe Asn Ile Ile Ser Pro Ser  
20 25 30  
Asn Asn Gly Gly Asn Val Gln Glu Thr Val Thr Ile Asp Asn Glu  
35 40 45  
Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser  
50 55 60  
Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val  
65 70 75  
Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn  
80 85 90

Ile	Pro	Pro	Leu	Asn	Asn	Leu	Gln	Trp	Tyr	Ile	Tyr	Glu	Lys	Gln
				95					100					105
Ala	Leu	Asp	Asn	Met	Phe	Ser	Asn	Lys	Tyr	Thr	Trp	Val	Lys	Tyr
				110					115					120
Asn	Pro	Leu	Glu	Ser	Leu	Ile	Lys	Asp	Val	Asp	Trp	Phe	Leu	Leu
				125					130					135
Gly	Ser	Pro	Ile	Glu	Lys	Leu	Cys	Lys	His	Ile	Pro	Leu	Tyr	Lys
				140					145					150
Gly	Glu	Val	Val	Glu	Asn	Thr	His	Asn	Val	Gly	Ala	Gly	Gly	Cys
				155					160					165
Ala	Lys	Ala	Gly	Leu	Leu	Gly	Ile	Leu	Gly	Ile	Ser	Ile	Cys	Ala
				170					175					180

Asp Ile His Val

<210> 222  
 <211> 992  
 <212> DNA  
 <213> Homo sapiens

<400> 222  
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 acccaccgag gcatggggct ccttgggctg ttctgcttgg ccgtgctggc 100  
 tgccagcagc ttctccaagg cacgggagga agaaattacc cctgtggtct 150  
 ccattgccta caaagtcctg gaagttttcc ccaaaggccg ctgggtgctc 200  
 ataacctgct gtgcacccca gccaccaccg cccatcacct attccctctg 250  
 tggaaccaag aacatcaagg tggccaagaa ggtggtgaag acccagcagc 300  
 cggcctcctt caacctcaac gtcacactca agtccagtcc agacctgctc 350  
 acctacttct gccgggctc ctccacctca ggtgcccattg tggacagtgc 400  
 caggctacag atgcactggg agctgtggtc caagccagtg tctgagctgc 450  
 gggccaactt cactctgcag gacagagggg caggccccag ggtggagatg 500  
 atctgccagg cgtcctcggg cagcccacct atcaccaaca gcctgatcgg 550  
 gaaggatggg caggtccacc tgcagcagag accatgccac aggcagcctg 600  
 ccaactttct cttcctgccg agccagacat cggactggtt ctggtgccag 650  
 gctgcaaaca acgccaatgt ccagcacagc gccctcacag tgggtgcccc 700  
 aggtggtgac cagaagatgg aggactggca gggctcccctg gagagcccca 750  
 tccttgctt gccgctctac aggagcacc gccgtctgag tgaagaggag 800  
 tttggggggt tcaggatagg gaatggggag gtcagaggac gcaaagcagc 850  
 agccatgtag aatgaaccgt ccagagagcc aagcacggca gaggactgca 900

ggccatcagc gtgcactgtt cgtatttga gttcatgcaa aatgagtgtg 950

ttttagctgc tcttgccaca aaaaaaaaaa aaaaaaaaaa aa 992

<210> 223

<211> 265

<212> PRT

<213> Homo sapiens

<400> 223

Met	Gly	Leu	Pro	Gly	Leu	Phe	Cys	Leu	Ala	Val	Leu	Ala	Ala	Ser	
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Ser	Phe	Ser	Lys	Ala	Arg	Glu	Glu	Glu	Ile	Thr	Pro	Val	Val	Ser	
				20					25					30	
Ile	Ala	Tyr	Lys	Val	Leu	Glu	Val	Phe	Pro	Lys	Gly	Arg	Trp	Val	
				35					40					45	
Leu	Ile	Thr	Cys	Cys	Ala	Pro	Gln	Pro	Pro	Pro	Pro	Ile	Thr	Tyr	
				50					55					60	
Ser	Leu	Cys	Gly	Thr	Lys	Asn	Ile	Lys	Val	Ala	Lys	Lys	Val	Val	
				65					70					75	
Lys	Thr	His	Glu	Pro	Ala	Ser	Phe	Asn	Leu	Asn	Val	Thr	Leu	Lys	
				80					85					90	
Ser	Ser	Pro	Asp	Leu	Leu	Thr	Tyr	Phe	Cys	Arg	Ala	Ser	Ser	Thr	
				95					100					105	
Ser	Gly	Ala	His	Val	Asp	Ser	Ala	Arg	Leu	Gln	Met	His	Trp	Glu	
				110					115					120	
Leu	Trp	Ser	Lys	Pro	Val	Ser	Glu	Leu	Arg	Ala	Asn	Phe	Thr	Leu	
				125					130					135	
Gln	Asp	Arg	Gly	Ala	Gly	Pro	Arg	Val	Glu	Met	Ile	Cys	Gln	Ala	
				140					145					150	
Ser	Ser	Gly	Ser	Pro	Pro	Ile	Thr	Asn	Ser	Leu	Ile	Gly	Lys	Asp	
				155					160					165	
Gly	Gln	Val	His	Leu	Gln	Gln	Arg	Pro	Cys	His	Arg	Gln	Pro	Ala	
				170					175					180	
Asn	Phe	Ser	Phe	Leu	Pro	Ser	Gln	Thr	Ser	Asp	Trp	Phe	Trp	Cys	
				185					190					195	
Gln	Ala	Ala	Asn	Asn	Ala	Asn	Val	Gln	His	Ser	Ala	Leu	Thr	Val	
				200					205					210	
Val	Pro	Pro	Gly	Gly	Asp	Gln	Lys	Met	Glu	Asp	Trp	Gln	Gly	Pro	
				215					220					225	
Leu	Glu	Ser	Pro	Ile	Leu	Ala	Leu	Pro	Leu	Tyr	Arg	Ser	Thr	Arg	
				230					235					240	
Arg	Leu	Ser	Glu	Glu	Glu	Phe	Gly	Gly	Phe	Arg	Ile	Gly	Asn	Gly	
				245					250					255	
Glu	Val	Arg	Gly	Arg	Lys	Ala	Ala	Ala	Met						
				260					265						

<210> 224  
<211> 1297  
<212> DNA  
<213> Homo sapiens

<400> 224  
ggtccttaat ggcagcagcc gccgctacca agatccttct gtgcctcccg 50  
cttctgctcc tgctgtccgg ctggtcccgg gctgggcgag ccgaccctca 100  
ctctctttgc tatgacatca ccgtcatccc taagttcaga cctggaccac 150  
ggtggtgtgc ggttcaaggc cagggtgatg aaaagacttt tcttcactat 200  
gactgtggca acaagacagt cacacctgtc agtcccctgg ggaagaaact 250  
aaatgtcaca acggcctgga aagcacagaa cccagtactg agagaggtgg 300  
tggacatact tacagagcaa ctgctgaca ttcagctgga gaattacaca 350  
cccaaggaac ccctcacct gcaggcaagg atgtcttgat agcagaaagc 400  
tgaaggacac agcagtggat cttggcagtt cagtttcgat gggcagatct 450  
tcctcctctt tgactcagag aagagaatgt ggacaacggt tcatcctgga 500  
gccagaaaga tgaaagaaaa gtgggagaat gacaagggtg tggccatgtc 550  
cttccattac ttctcaatgg gagactgtat aggatggctt gaggaacttct 600  
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agcacggtct tgatcaaaact cgccttctg tctggccagc tgccaacgac 850  
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ccaatagctc attcactgcc ttgattcctt ttgccaacaa ttttaccagc 950  
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ttcctgcact taaagttctg gctgactaaa caagatatat catcttcttt 1050  
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tggggattct ttccgtgtcc tgaaagagaa tttttaaaatt atttaataag 1200  
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<210> 225  
<211> 246  
<212> PRT  
<213> Homo sapiens

<400> 225

Met	Ala	Ala	Ala	Ala	Ala	Thr	Lys	Ile	Leu	Leu	Cys	Leu	Pro	Leu	
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Leu	Leu	Leu	Leu	Ser	Gly	Trp	Ser	Arg	Ala	Gly	Arg	Ala	Asp	Pro	
				20					25					30	
His	Ser	Leu	Cys	Tyr	Asp	Ile	Thr	Val	Ile	Pro	Lys	Phe	Arg	Pro	
				35					40					45	
Gly	Pro	Arg	Trp	Cys	Ala	Val	Gln	Gly	Gln	Val	Asp	Glu	Lys	Thr	
				50					55					60	
Phe	Leu	His	Tyr	Asp	Cys	Gly	Asn	Lys	Thr	Val	Thr	Pro	Val	Ser	
				65					70					75	
Pro	Leu	Gly	Lys	Lys	Leu	Asn	Val	Thr	Thr	Ala	Trp	Lys	Ala	Gln	
				80					85					90	
Asn	Pro	Val	Leu	Arg	Glu	Val	Val	Asp	Ile	Leu	Thr	Glu	Gln	Leu	
				95					100					105	
Arg	Asp	Ile	Gln	Leu	Glu	Asn	Tyr	Thr	Pro	Lys	Glu	Pro	Leu	Thr	
				110					115					120	
Leu	Gln	Ala	Arg	Met	Ser	Cys	Glu	Gln	Lys	Ala	Glu	Gly	His	Ser	
				125					130					135	
Ser	Gly	Ser	Trp	Gln	Phe	Ser	Phe	Asp	Gly	Gln	Ile	Phe	Leu	Leu	
				140					145					150	
Phe	Asp	Ser	Glu	Lys	Arg	Met	Trp	Thr	Thr	Val	His	Pro	Gly	Ala	
				155					160					165	
Arg	Lys	Met	Lys	Glu	Lys	Trp	Glu	Asn	Asp	Lys	Val	Val	Ala	Met	
				170					175					180	
Ser	Phe	His	Tyr	Phe	Ser	Met	Gly	Asp	Cys	Ile	Gly	Trp	Leu	Glu	
				185					190					195	
Asp	Phe	Leu	Met	Gly	Met	Asp	Ser	Thr	Leu	Glu	Pro	Ser	Ala	Gly	
				200					205					210	
Ala	Pro	Leu	Ala	Met	Ser	Ser	Gly	Thr	Thr	Gln	Leu	Arg	Ala	Thr	
				215					220					225	
Ala	Thr	Thr	Leu	Ile	Leu	Cys	Cys	Leu	Leu	Ile	Ile	Leu	Pro	Cys	
				230					235					240	
Phe	Ile	Leu	Pro	Gly	Ile										
				245											

<210> 226

<211> 735

<212> DNA

<213> Homo sapiens

<400> 226

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caagttatat accgtggaat ggagttgatc ccaaccataa catcgtggag 150

ggttttaatt ttggtagtag ccctcaccaca attctggtgt ggctttcttt 200  
 gcagaggatt ccaccttcaa aatcatgaac tctggctggt gatcaaaaga 250  
 gaatttggtat tctactctaa aagtcaatat aggacttggc aaaagaagct 300  
 agcagaagac tcaacctggc ctcccataaa caggacagat tattcaggtg 350  
 atggcaaaaa tggattctac atcaacggag gctatgaaag ccatgaacag 400  
 attccaaaaa gaaaactcaa attgggagggc caaccacag aacagcattt 450  
 ctggggccagg ctgtaatcag aattgtcgtc gtacatgctc aacagcattg 500  
 cttttttccc caaaattaac acattgtgga gaagtgatga tactctcccc 550  
 ttacctttcc tctctccatt caagcattca aagtatattt tcaatgaatt 600  
 aaaccttgca gcaagggacc ttagatagggc ttattctgac tgtatgcttt 650  
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 gtattcattt tgaaaaaaaa aaaaaaaaaa aaaaa 735

<210> 227  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 227  
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 Val Val Ala Leu Thr Gln Phe Trp Cys Gly Phe Leu Cys Arg Gly  
 20 25 30  
 Phe His Leu Gln Asn His Glu Leu Trp Leu Leu Ile Lys Arg Glu  
 35 40 45  
 Phe Gly Phe Tyr Ser Lys Ser Gln Tyr Arg Thr Trp Gln Lys Lys  
 50 55 60  
 Leu Ala Glu Asp Ser Thr Trp Pro Pro Ile Asn Arg Thr Asp Tyr  
 65 70 75  
 Ser Gly Asp Gly Lys Asn Gly Phe Tyr Ile Asn Gly Gly Tyr Glu  
 80 85 90  
 Ser His Glu Gln Ile Pro Lys Arg Lys Leu Lys Leu Gly Gly Gln  
 95 100 105  
 Pro Thr Glu Gln His Phe Trp Ala Arg Leu  
 110 115

<210> 228  
 <211> 2185  
 <212> DNA  
 <213> Homo sapiens

<400> 228  
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 cacaccatga agctcttgtg gcaggtaact gtgcaccacc acacctggaa 100

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 gtgcagccat cgctgctgcc gcctcagccg ggccccagaa ctgcccctcc 200  
 gtttgctcgt gcagtaacca gttcagcaag gtggtgtgca cgcgccgggg 250  
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 tcatggagaa caacatccag atgatccagg ccgacacctt ccgccacctc 350  
 caccacctgg aggtcctgca gttgggcagg aactccatcc ggcagattga 400  
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 cgccttcaac cgggtgccct ccctcatgcg cctggacttg ggggagctca 600  
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 tcgagagtat ataccacca attccacctg ctgtggccgc tgtcatgctc 1050  
 ccatgcacat gcgaggccgc tacctcgtgg aggtggacca ggctccttc 1100  
 cagtgcctcg ccccttcat catggacgca cctcgagacc tcaacatttc 1150  
 tgagggtcgg atggcagaac ttaagtgtcg gactccccct atgtcctccg 1200  
 tgaagtgggt gctgccaat gggacagtgc tcagccacgc ctcccgcac 1250  
 ccaaggatct ctgtcctcaa cgacggcacc ttgaactttt cccacgtgct 1300  
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 tccaactaca gcttcttcac cacagtaaca gtggagacca cggagatctc 1450  
 gcctgaggac acaacgcgaa agtacaagcc tgttcctacc acgtccactg 1500  
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 gcagaccagc ctggatgaag tcatgaagac caccaagatc atcattggct 1650  
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 cagcaacagc agctccgtcc ggtgtatcag gtgagggggc agtagtgctg 1850  
 cccacaattc atgaccatat taactacaac acctacaaac cagcacatgg 1900  
 ggcccactgg acagaaaaca gcctggggaa ctctctgcac cccacagtca 1950  
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 caggaaactc aaatatgact cccctcccc aaaaaactta taaaatgcaa 2050  
 tagaatgcac acaaagacag caacttttgt acagagtggg gagagacttt 2100  
 ttcttgtata tgcttatata ttaagtctat gggctggtta aaaaaaacag 2150  
 attatattaa aatttaaaga caaaaagtca aaaca 2185

<210> 229

<211> 653

<212> PRT

<213> Homo sapiens

<400> 229

Met	Lys	Leu	Leu	Trp	Gln	Val	Thr	Val	His	His	His	Thr	Trp	Asn
1				5					10					15
Ala	Ile	Leu	Leu	Pro	Phe	Val	Tyr	Leu	Thr	Ala	Gln	Val	Trp	Ile
				20					25					30
Leu	Cys	Ala	Ala	Ile	Ala	Ala	Ala	Ala	Ser	Ala	Gly	Pro	Gln	Asn
				35					40					45
Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val	Val
				50					55					60
Cys	Thr	Arg	Arg	Gly	Leu	Ser	Glu	Val	Pro	Gln	Gly	Ile	Pro	Ser
				65					70					75
Asn	Thr	Arg	Tyr	Leu	Asn	Leu	Met	Glu	Asn	Asn	Ile	Gln	Met	Ile
				80					85					90
Gln	Ala	Asp	Thr	Phe	Arg	His	Leu	His	His	Leu	Glu	Val	Leu	Gln
				95					100					105
Leu	Gly	Arg	Asn	Ser	Ile	Arg	Gln	Ile	Glu	Val	Gly	Ala	Phe	Asn
				110					115					120
Gly	Leu	Ala	Ser	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Trp	Leu
				125					130					135
Thr	Val	Ile	Pro	Ser	Gly	Ala	Phe	Glu	Tyr	Leu	Ser	Lys	Leu	Arg
				140					145					150
Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser	Tyr
				155					160					165
Ala	Phe	Asn	Arg	Val	Pro	Ser	Leu	Met	Arg	Leu	Asp	Leu	Gly	Glu
				170					175					180
Leu	Lys	Lys	Leu	Glu	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	Glu	Gly	Leu

185					190					195				
Phe	Asn	Leu	Lys	Tyr	Leu	Asn	Leu	Gly	Met	Cys	Asn	Ile	Lys	Asp
				200					205					210
Met	Pro	Asn	Leu	Thr	Pro	Leu	Val	Gly	Leu	Glu	Glu	Leu	Glu	Met
				215					220					225
Ser	Gly	Asn	His	Phe	Pro	Glu	Ile	Arg	Pro	Gly	Ser	Phe	His	Gly
				230					235					240
Leu	Ser	Ser	Leu	Lys	Lys	Leu	Trp	Val	Met	Asn	Ser	Gln	Val	Ser
				245					250					255
Leu	Ile	Glu	Arg	Asn	Ala	Phe	Asp	Gly	Leu	Ala	Ser	Leu	Val	Glu
				260					265					270
Leu	Asn	Leu	Ala	His	Asn	Asn	Leu	Ser	Ser	Leu	Pro	His	Asp	Leu
				275					280					285
Phe	Thr	Pro	Leu	Arg	Tyr	Leu	Val	Glu	Leu	His	Leu	His	His	Asn
				290					295					300
Pro	Trp	Asn	Cys	Asp	Cys	Asp	Ile	Leu	Trp	Leu	Ala	Trp	Trp	Leu
				305					310					315
Arg	Glu	Tyr	Ile	Pro	Thr	Asn	Ser	Thr	Cys	Cys	Gly	Arg	Cys	His
				320					325					330
Ala	Pro	Met	His	Met	Arg	Gly	Arg	Tyr	Leu	Val	Glu	Val	Asp	Gln
				335					340					345
Ala	Ser	Phe	Gln	Cys	Ser	Ala	Pro	Phe	Ile	Met	Asp	Ala	Pro	Arg
				350					355					360
Asp	Leu	Asn	Ile	Ser	Glu	Gly	Arg	Met	Ala	Glu	Leu	Lys	Cys	Arg
				365					370					375
Thr	Pro	Pro	Met	Ser	Ser	Val	Lys	Trp	Leu	Leu	Pro	Asn	Gly	Thr
				380					385					390
Val	Leu	Ser	His	Ala	Ser	Arg	His	Pro	Arg	Ile	Ser	Val	Leu	Asn
				395					400					405
Asp	Gly	Thr	Leu	Asn	Phe	Ser	His	Val	Leu	Leu	Ser	Asp	Thr	Gly
				410					415					420
Val	Tyr	Thr	Cys	Met	Val	Thr	Asn	Val	Ala	Gly	Asn	Ser	Asn	Ala
				425					430					435
Ser	Ala	Tyr	Leu	Asn	Val	Ser	Thr	Ala	Glu	Leu	Asn	Thr	Ser	Asn
				440					445					450
Tyr	Ser	Phe	Phe	Thr	Thr	Val	Thr	Val	Glu	Thr	Thr	Glu	Ile	Ser
				455					460					465
Pro	Glu	Asp	Thr	Thr	Arg	Lys	Tyr	Lys	Pro	Val	Pro	Thr	Thr	Ser
				470					475					480
Thr	Gly	Tyr	Gln	Pro	Ala	Tyr	Thr	Thr	Ser	Thr	Thr	Val	Leu	Ile
				485					490					495
Gln	Thr	Thr	Arg	Val	Pro	Lys	Gln	Val	Ala	Val	Pro	Ala	Thr	Asp

	500	505	510
Thr Thr Asp Lys	Met Gln Thr Ser Leu	Asp Glu Val Met Lys	Thr
	515	520	525
Thr Lys Ile Ile	Ile Gly Cys Phe Val	Ala Val Thr Leu Leu	Ala
	530	535	540
Ala Ala Met Leu	Ile Val Phe Tyr Lys	Leu Arg Lys Arg His	Gln
	545	550	555
Gln Arg Ser Thr	Val Thr Ala Ala Arg	Thr Val Glu Ile Ile	Gln
	560	565	570
Val Asp Glu Asp	Ile Pro Ala Ala Thr	Ser Ala Ala Ala Thr	Ala
	575	580	585
Ala Pro Ser Gly	Val Ser Gly Glu Gly	Ala Val Val Leu Pro	Thr
	590	595	600
Ile His Asp His	Ile Asn Tyr Asn Thr	Tyr Lys Pro Ala His	Gly
	605	610	615
Ala His Trp Thr	Glu Asn Ser Leu Gly	Asn Ser Leu His Pro	Thr
	620	625	630
Val Thr Thr Ile	Ser Glu Pro Tyr Ile	Ile Gln Thr His Thr	Lys
	635	640	645
Asp Lys Val Gln	Glu Thr Gln Ile		
	650		

<210> 230  
 <211> 2846  
 <212> DNA  
 <213> Homo sapiens

<400> 230  
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 tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg 150  
 tcgggagtgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga 200  
 gggaagtctg gggtataacc atcccttgct gcaggaatga ggagaatgag 250  
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 gagctgccga aatggctcat gggggggtac cttggatgac ttctatgtga 350  
 aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc 400  
 atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttgga 450  
 aagctatccc ctaaagtctc actgtgaatg gaccattcat gctaaacctg 500  
 ggtttgcac ccaactaaga tttgtcatgt tgagtctgga gtttgactac 550  
 atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcgatgg 600  
 ccagatcatc aagcgtgtct gtggcaacga gggccagct cctatccaga 650

goataggatc ctcaactccac gtccctcttcc actccgatgg ctccaagaat 700  
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 cccttgtttc catgacggca cgtgcgtcct tgacaaggct ggatcctaca 800  
 agtgtgcctg cttggcaggc tatactgggc agcgcctgtga aaatctcctt 850  
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 aaaagaactt gccagcagaa tggagagtgg tcaggggaaac agcccatctg 1050  
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<210> 231  
<211> 720  
<212> PRT  
<213> Homo sapiens

<400> 231  
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Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys  
35 40 45  
Cys Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu  
50 55 60  
Val Val Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu  
65 70 75  
Cys Asp Ser Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn  
80 85 90  
Cys Lys Ser Cys Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp  
95 100 105  
Phe Tyr Val Lys Gly Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp  
110 115 120  
Tyr Gly Gly Asp Cys Met Arg Cys Gly Gln Val Leu Arg Ala Pro  
125 130 135  
Lys Gly Gln Ile Leu Leu Glu Ser Tyr Pro Leu Asn Ala His Cys  
140 145 150  
Glu Trp Thr Ile His Ala Lys Pro Gly Phe Val Ile Gln Leu Arg  
155 160 165

Phe Val Met Leu Ser	Leu Glu Phe Asp	Tyr Met Cys Gln Tyr Asp	170	175	180
Tyr Val Glu Val Arg	Asp Gly Asp Asn	Arg Asp Gly Gln Ile Ile	185	190	195
Lys Arg Val Cys Gly	Asn Glu Arg Pro	Ala Pro Ile Gln Ser Ile	200	205	210
Gly Ser Ser Leu His	Val Leu Phe His	Ser Asp Gly Ser Lys Asn	215	220	225
Phe Asp Gly Phe His	Ala Ile Tyr Glu	Glu Ile Thr Ala Cys Ser	230	235	240
Ser Ser Pro Cys Phe	His Asp Gly Thr	Cys Val Leu Asp Lys Ala	245	250	255
Gly Ser Tyr Lys Cys	Ala Cys Leu Ala	Gly Tyr Thr Gly Gln Arg	260	265	270
Cys Glu Asn Leu Leu	Glu Glu Arg Asn	Cys Ser Asp Pro Gly Gly	275	280	285
Pro Val Asn Gly Tyr	Gln Lys Ile Thr	Gly Gly Pro Gly Leu Ile	290	295	300
Asn Gly Arg His Ala	Lys Ile Gly Thr	Val Val Ser Phe Phe Cys	305	310	315
Asn Asn Ser Tyr Val	Leu Ser Gly Asn	Glu Lys Arg Thr Cys Gln	320	325	330
Gln Asn Gly Glu Trp	Ser Gly Lys Gln	Pro Ile Cys Ile Lys Ala	335	340	345
Cys Arg Glu Pro Lys	Ile Ser Asp Leu	Val Arg Arg Arg Val Leu	350	355	360
Pro Met Gln Val Gln	Ser Arg Glu Thr	Pro Leu His Gln Leu Tyr	365	370	375
Ser Ala Ala Phe Ser	Lys Gln Lys Leu	Gln Ser Ala Pro Thr Lys	380	385	390
Lys Pro Ala Leu Pro	Phe Gly Asp Leu	Pro Met Gly Tyr Gln His	395	400	405
Leu His Thr Gln Leu	Gln Tyr Glu Cys	Ile Ser Pro Phe Tyr Arg	410	415	420
Arg Leu Gly Ser Ser	Arg Arg Thr Cys	Leu Arg Thr Gly Lys Trp	425	430	435
Ser Gly Arg Ala Pro	Ser Cys Ile Pro	Ile Cys Gly Lys Ile Glu	440	445	450
Asn Ile Thr Ala Pro	Lys Thr Gln Gly	Leu Arg Trp Pro Trp Gln	455	460	465
Ala Ala Ile Tyr Arg	Arg Thr Ser Gly	Val His Asp Gly Ser Leu	470	475	480

His	Lys	Gly	Ala	Trp	Phe	Leu	Val	Cys	Ser	Gly	Ala	Leu	Val	Asn
				485					490					495
Glu	Arg	Thr	Val	Val	Val	Ala	Ala	His	Cys	Val	Thr	Asp	Leu	Gly
				500					505					510
Lys	Val	Thr	Met	Ile	Lys	Thr	Ala	Asp	Leu	Lys	Val	Val	Leu	Gly
				515					520					525
Lys	Phe	Tyr	Arg	Asp	Asp	Asp	Arg	Asp	Glu	Lys	Thr	Ile	Gln	Ser
				530					535					540
Leu	Gln	Ile	Ser	Ala	Ile	Ile	Leu	His	Pro	Asn	Tyr	Asp	Pro	Ile
				545					550					555
Leu	Leu	Asp	Ala	Asp	Ile	Ala	Ile	Leu	Lys	Leu	Leu	Asp	Lys	Ala
				560					565					570
Arg	Ile	Ser	Thr	Arg	Val	Gln	Pro	Ile	Cys	Leu	Ala	Ala	Ser	Arg
				575					580					585
Asp	Leu	Ser	Thr	Ser	Phe	Gln	Glu	Ser	His	Ile	Thr	Val	Ala	Gly
				590					595					600
Trp	Asn	Val	Leu	Ala	Asp	Val	Arg	Ser	Pro	Gly	Phe	Lys	Asn	Asp
				605					610					615
Thr	Leu	Arg	Ser	Gly	Val	Val	Ser	Val	Val	Asp	Ser	Leu	Leu	Cys
				620					625					630
Glu	Glu	Gln	His	Glu	Asp	His	Gly	Ile	Pro	Val	Ser	Val	Thr	Asp
				635					640					645
Asn	Met	Phe	Cys	Ala	Ser	Trp	Glu	Pro	Thr	Ala	Pro	Ser	Asp	Ile
				650					655					660
Cys	Thr	Ala	Glu	Thr	Gly	Gly	Ile	Ala	Ala	Val	Ser	Phe	Pro	Gly
				665					670					675
Arg	Ala	Ser	Pro	Glu	Pro	Arg	Trp	His	Leu	Met	Gly	Leu	Val	Ser
				680					685					690
Trp	Ser	Tyr	Asp	Lys	Thr	Cys	Ser	His	Arg	Leu	Ser	Thr	Ala	Phe
				695					700					705
Thr	Lys	Val	Leu	Pro	Phe	Lys	Asp	Trp	Ile	Glu	Arg	Asn	Met	Lys
				710					715					720

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

aggttcgtga tggagacaac cgcg 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 233  
tgtcaaggac gcactgccgt catg 24

<210> 234  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 234  
tggccagatc atcaagcgtg tctgtggcaa cgagcggcca gtcctatcc 50

<210> 235  
<211> 1964  
<212> DNA  
<213> Homo sapiens

<400> 235  
accaggcatt gtatcttcag ttgtcatcaa gttcgcaatc agattggaaa 50  
agctcaactt gaagctttct tgcctgcagt gaagcagaga gatagatatt 100  
attcacgtaa taaaaaacat gggcttcaac ctgactttcc acctttccta 150  
caaattccga ttactgttgc tgttgacttt gtgcctgaca gtggttgggt 200  
gggccaccag taactacttc gtgggtgcca ttcaagagat tcctaaagca 250  
aaggagtcca tggctaattt ccataagacc ctcatTTTtg ggaaggga 300  
aactctgact aatgaagcat ccacgaagaa ggtagaactt gacaactgtc 350  
cttctgtgtc tccttacctc agaggccaga gcaagctcat tttcaaacca 400  
gatctcactt tggaagaggt acaggcagaa aatcccaaag tgtccagagg 450  
ccggtatcgc cctcaggaat gtaaagcttt acagagggtc gccatcctcg 500  
ttccccaccg gaacagagag aaacacctga tgtacctgct ggaacatctg 550  
catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca 600  
ccaggctgaa ggtaaaaagt ttaatogagc caaactcttg aatgtgggt 650  
atctagaagc cctcaaggaa gaaaattggg actgctttat attccacgat 700  
gtggacctgg taccgagaa tgactttaac ctttacaagt gtgaggagca 750  
tccaagcat ctggtggttg gcaggaacag cactgggtac aggttacgtt 800  
acagtggata ttttgggggt gttactgcc taagcagaga gcagtttttc 850  
aaggatgaatg gattctctaa caactactgg ggatggggag gcgaagacga 900  
tgacctcaga ctcagggttg agctccaaag aatgaaaatt tcccgcccc 950  
tgctgaagt gggtaaatat acaatggtct tccacactag agacaaaggc 1000

aatgagggtga acgcagaacg gatgaagctc ttacaccaag tgtcacgagt 1050  
ctggagaaca gatgggttga gtagttgttc ttataaatta gtatctgtgg 1100  
aacacaatcc tttatatatc aacatcacag tggatttctg gtttggtgca 1150  
tgaccctgga tcttttggtg atgtttggaa gaactgattc tttgtttgca 1200  
ataattttgg cctagagact tcaaatagta gcacacatta agaacctgtt 1250  
acagctcatt gttgagctga atttttcctt tttgtatttt cttagcagag 1300  
ctcctggtga tgtagagtat aaaacagttg taacaagaca gctttcttag 1350  
tcattttgat catgagggtt aaatattgta atatggatac ttgaaggact 1400  
ttatataaaa ggatgactca aaggataaaa tgaacgctat ttgaggactc 1450  
tggttgaagg agatttattt aaatttgaag taatatatta tgggataaaa 1500  
ggccacagga aataagactg ctgaatgtct gagagaacca gagttgttct 1550  
cgtccaaggt agaaaggtag gaagatacaa tactgttatt cattttatcct 1600  
gtacaatcat ctgtgaagtg gtggtgtcag gtgagaaggc gtccacaaaa 1650  
gaggggagaa aaggcgacga atcaggacac agtgaacttg ggaatgaaga 1700  
ggtagcagga ggggtggagtg tcggctgcaa aggcagcagt agctgagctg 1750  
gttgacaggt ctgatagcct tcaggggagg acctgcccag gtatgccttc 1800  
cagtgatgcc caccagagaa tacattctct attagttttt aaagagtttt 1850  
tgtaaaatga ttttgtacaa gtaggatatg aattagcagt ttacaagttt 1900  
acatattaac taataataaa tatgtctatc aaatacctct gtagtaaaat 1950  
gtgaaaaagc aaaa 1964

<210> 236  
<211> 344  
<212> PRT  
<213> Homo sapiens

<220>  
<221> Signal peptide  
<222> 1-27  
<223> Signal peptide

<220>  
<221> N-glycosylation sites  
<222> 4-7, 220-223, 335-338  
<223> N-glycosylation sites

<220>  
<221> Xylose isomerase proteins  
<222> 191-201  
<223> Xylose isomerase proteins

<400> 236  
Met Gly Phe Asn Leu Thr Phe His Leu Ser Tyr Lys Phe Arg Leu  
1 5 10 15

Leu	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Val	Val	Gly	Trp	Ala	Thr	
				20					25					30	
Ser	Asn	Tyr	Phe	Val	Gly	Ala	Ile	Gln	Glu	Ile	Pro	Lys	Ala	Lys	
				35					40					45	
Glu	Phe	Met	Ala	Asn	Phe	His	Lys	Thr	Leu	Ile	Leu	Gly	Lys	Gly	
				50					55					60	
Lys	Thr	Leu	Thr	Asn	Glu	Ala	Ser	Thr	Lys	Lys	Val	Glu	Leu	Asp	
				65					70					75	
Asn	Cys	Pro	Ser	Val	Ser	Pro	Tyr	Leu	Arg	Gly	Gln	Ser	Lys	Leu	
				80					85					90	
Ile	Phe	Lys	Pro	Asp	Leu	Thr	Leu	Glu	Glu	Val	Gln	Ala	Glu	Asn	
				95					100					105	
Pro	Lys	Val	Ser	Arg	Gly	Arg	Tyr	Arg	Pro	Gln	Glu	Cys	Lys	Ala	
				110					115					120	
Leu	Gln	Arg	Val	Ala	Ile	Leu	Val	Pro	His	Arg	Asn	Arg	Glu	Lys	
				125					130					135	
His	Leu	Met	Tyr	Leu	Leu	Glu	His	Leu	His	Pro	Phe	Leu	Gln	Arg	
				140					145					150	
Gln	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	His	Gln	Ala	Glu	Gly	
				155					160					165	
Lys	Ly's	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	Val	Gly	Tyr	Leu	Glu	
				170					175					180	
Ala	Leu	Lys	Glu	Glu	Asn	Trp	Asp	Cys	Phe	Ile	Phe	His	Asp	Val	
				185					190					195	
Asp	Leu	Val	Pro	Glu	Asn	Asp	Phe	Asn	Leu	Tyr	Lys	Cys	Glu	Glu	
				200					205					210	
His	Pro	Lys	His	Leu	Val	Val	Gly	Arg	Asn	Ser	Thr	Gly	Tyr	Arg	
				215					220					225	
Leu	Arg	Tyr	Ser	Gly	Tyr	Phe	Gly	Gly	Val	Thr	Ala	Leu	Ser	Arg	
				230					235					240	
Glu	Gln	Phe	Phe	Lys	Val	Asn	Gly	Phe	Ser	Asn	Asn	Tyr	Trp	Gly	
				245					250					255	
Trp	Gly	Gly	Glu	Asp	Asp	Asp	Leu	Arg	Leu	Arg	Val	Glu	Leu	Gln	
				260					265					270	
Arg	Met	Lys	Ile	Ser	Arg	Pro	Leu	Pro	Glu	Val	Gly	Lys	Tyr	Thr	
				275					280					285	
Met	Val	Phe	His	Thr	Arg	Asp	Lys	Gly	Asn	Glu	Val	Asn	Ala	Glu	
				290					295					300	
Arg	Met	Lys	Leu	Leu	His	Gln	Val	Ser	Arg	Val	Trp	Arg	Thr	Asp	
				305					310					315	
Gly	Leu	Ser	Ser	Cys	Ser	Tyr	Lys	Leu	Val	Ser	Val	Glu	His	Asn	
				320					325					330	

Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala  
 335 340

<210> 237  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 237  
 ccttacctca gaggccagag caagc 25

<210> 238  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 238  
 gagcttcacg cgttctgcgt tcacc 25

<210> 239  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 239  
 caggaatgta aagctttaca gagggctgcc atcctcgttc cccacc 46

<210> 240  
 <211> 2567  
 <212> DNA  
 <213> Homo sapiens

<400> 240  
 cgtgggccgg ggtcgcgcag cgggctgtgg gcgcgcccg aggagcgacc 50  
 gccgcagttc tcgagctcca gctgcattcc ctccgcgtcc gcccacgct 100  
 tctcccgctc cggggcccgcc aatggcccag gcagtgtggt cgcgcctcgg 150  
 ccgcaccttc tggtttgctt gctcctgcc ctggggcccg gcaggggtgg 200  
 ccgcaggcct gtatgaactc aatctcacca ccgatagccc tgccaccacg 250  
 ggagcggtgg tgaccatctc ggccagcctg gtggccaagg acaacggcag 300  
 cctggccctg cccgctgacg cccacctcta ccgcttcac tggtaccaca 350  
 ccccgctggt gcttactggc aagatggaga agggctctag ctccaccatc 400  
 cgtgtggtcg gccacgtgcc cggggaattc ccggtctctg tctgggtcac 450  
 tgccgctgac tgctggatgt gccagcctgt ggccaggggc tttgtggtcc 500  
 tccccatcac agagttctc gtgggggacc ttgttgcac ccagaacact 550

tccctaccct ggcccagctc ctatctcact aagaccgtcc tgaaagtctc 600  
 ctctctcctc cagcaccga gcaacttcct caagaccgcc ttgtttctct 650  
 acagctggga cttcggggac gggaccaga tggtgactga agactccgtg 700  
 gtctattata actattccat catcgggacc ttcaccgtga agctcaaagt 750  
 ggtggcggag tgggaagagg tggagccgga tgccacgagg gctgtgaagc 800  
 agaagaccgg ggacttctcc gcctcgtga agctgcagga aaccttcga 850  
 ggcatccaag tgttggggcc caccctaatt cagaccttc aaaagatgac 900  
 cgtgaccttg aacttcctgg ggagccctcc tctgactgtg tgctggcgtc 950  
 tcaagcctga gtgcctccc ctggagggaag gggagtgcc cctgtgtcc 1000  
 gtggccagca cagcgtacaa cctgaccac accttcaggg acctgggga 1050  
 ctactgcttc agcatccggg ccgagaatat catcagcaag acacatcagt 1100  
 accacaagat ccagggtgtg ccctccagaa tccagccggc tgtctttgct 1150  
 ttcccatgtg ctacacttat cactgtgatg ttggccttca tcatgtacat 1200  
 gacctgcgg aatgccactc agcaaaagga catggtggag aaccgggagc 1250  
 caccctctgg ggtcagggtc tgctgccaga tgtgctgtgg gcctttcttg 1300  
 ctggagactc catctgagta cctggaaatt gttcgtgaga accacgggct 1350  
 gctcccgccc ctctataagt ctgtcaaac ttacaccgtg tgagcactcc 1400  
 cctcccccac cccatctcag tgttaactga ctgctgactt ggagtttcca 1450  
 gcagggtggt gtgcaccact gaccaggagg ggttcatttg cgtggggctg 1500  
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 cctccctctc tgtcaccctc gacccagcc attcaccat ctgtacagtc 1600  
 cagccactga cataagcccc actcggttac caccctctg acccctacc 1650  
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 ctctagggtg ggctgggtg cccactgcc attcctctca tattggcaca 1750  
 tctgctgtcc attgggggtt ctgagtttcc tccccagac agccctacct 1800  
 gtgccagaga gctagaaaga aggtcataaa gggttaaaaa tccataacta 1850  
 aaggttgtac acatagatgg gcacactcac agagagaagt gtgcatgtac 1900  
 acacaccaca cacacacaca cacacacaca cacagaaata taaacacatg 1950  
 cgtcacatgg gcatttcaga tgatcagctc tgtatctggt taagtogggt 2000  
 gctgggatgc accctgcact agagctgaaa ggaaatttga cctccaagca 2050  
 gccctgacag gttctgggccc cgggccctcc ctttgtgctt tgtctctgca 2100  
 gttcttgccc cctttataag gccatcctag tccctgctgg ctggcagggg 2150

cctggatggg gggcaggact aatactgagt gattgcagag tgctttataa 2200  
 atatcacctt attttatcga aaccatctg tgaaactttc actgaggaaa 2250  
 aggccttgca gcggtagaag aggttgagtc aaggccgggc gcggtggctc 2300  
 acgcctgtaa tcccagcact ttgggaggcc gaggcgggtg gatcacgaga 2350  
 tcaggagatc gagaccaccc tggctaacac ggtgaaaccc cgtctctact 2400  
 aaaaaaatac aaaaagttag ccgggcgtgg tgggtgggtgc ctgtagtccc 2450  
 agctactcgg gaggctgagg caggagaatg gtgcgaaccc gggaggcgga 2500  
 gcttgcaagt agcccagatg gcgccactgc actccagcct gagtgcacaga 2550  
 gcgagactct gtctcca 2567

<210> 241

<211> 423

<212> PRT

<213> Homo sapiens

<400> 241

Met	Ala	Gln	Ala	Val	Trp	Ser	Arg	Leu	Gly	Arg	Ile	Leu	Trp	Leu	1	5	10	15
Ala	Cys	Leu	Leu	Pro	Trp	Ala	Pro	Ala	Gly	Val	Ala	Ala	Gly	Leu	20	25	30	
Tyr	Glu	Leu	Asn	Leu	Thr	Thr	Asp	Ser	Pro	Ala	Thr	Thr	Gly	Ala	35	40	45	
Val	Val	Thr	Ile	Ser	Ala	Ser	Leu	Val	Ala	Lys	Asp	Asn	Gly	Ser	50	55	60	
Leu	Ala	Leu	Pro	Ala	Asp	Ala	His	Leu	Tyr	Arg	Phe	His	Trp	Ile	65	70	75	
His	Thr	Pro	Leu	Val	Leu	Thr	Gly	Lys	Met	Glu	Lys	Gly	Leu	Ser	80	85	90	
Ser	Thr	Ile	Arg	Val	Val	Gly	His	Val	Pro	Gly	Glu	Phe	Pro	Val	95	100	105	
Ser	Val	Trp	Val	Thr	Ala	Ala	Asp	Cys	Trp	Met	Cys	Gln	Pro	Val	110	115	120	
Ala	Arg	Gly	Phe	Val	Val	Leu	Pro	Ile	Thr	Glu	Phe	Leu	Val	Gly	125	130	135	
Asp	Leu	Val	Val	Thr	Gln	Asn	Thr	Ser	Leu	Pro	Trp	Pro	Ser	Ser	140	145	150	
Tyr	Leu	Thr	Lys	Thr	Val	Leu	Lys	Val	Ser	Phe	Leu	Leu	His	Asp	155	160	165	
Pro	Ser	Asn	Phe	Leu	Lys	Thr	Ala	Leu	Phe	Leu	Tyr	Ser	Trp	Asp	170	175	180	
Phe	Gly	Asp	Gly	Thr	Gln	Met	Val	Thr	Glu	Asp	Ser	Val	Val	Tyr	185	190	195	

Tyr	Asn	Tyr	Ser	Ile	Ile	Gly	Thr	Phe	Thr	Val	Lys	Leu	Lys	Val	
				200					205					210	
Val	Ala	Glu	Trp	Glu	Glu	Val	Glu	Pro	Asp	Ala	Thr	Arg	Ala	Val	
				215					220					225	
Lys	Gln	Lys	Thr	Gly	Asp	Phe	Ser	Ala	Ser	Leu	Lys	Leu	Gln	Glu	
				230					235					240	
Thr	Leu	Arg	Gly	Ile	Gln	Val	Leu	Gly	Pro	Thr	Leu	Ile	Gln	Thr	
				245					250					255	
Phe	Gln	Lys	Met	Thr	Val	Thr	Leu	Asn	Phe	Leu	Gly	Ser	Pro	Pro	
				260					265					270	
Leu	Thr	Val	Cys	Trp	Arg	Leu	Lys	Pro	Glu	Cys	Leu	Pro	Leu	Glu	
				275					280					285	
Glu	Gly	Glu	Cys	His	Pro	Val	Ser	Val	Ala	Ser	Thr	Ala	Tyr	Asn	
				290					295					300	
Leu	Thr	His	Thr	Phe	Arg	Asp	Pro	Gly	Asp	Tyr	Cys	Phe	Ser	Ile	
				305					310					315	
Arg	Ala	Glu	Asn	Ile	Ile	Ser	Lys	Thr	His	Gln	Tyr	His	Lys	Ile	
				320					325					330	
Gln	Val	Trp	Pro	Ser	Arg	Ile	Gln	Pro	Ala	Val	Phe	Ala	Phe	Pro	
				335					340					345	
Cys	Ala	Thr	Leu	Ile	Thr	Val	Met	Leu	Ala	Phe	Ile	Met	Tyr	Met	
				350					355					360	
Thr	Leu	Arg	Asn	Ala	Thr	Gln	Gln	Lys	Asp	Met	Val	Glu	Asn	Pro	
				365					370					375	
Glu	Pro	Pro	Ser	Gly	Val	Arg	Cys	Cys	Cys	Gln	Met	Cys	Cys	Gly	
				380					385					390	
Pro	Phe	Leu	Leu	Glu	Thr	Pro	Ser	Glu	Tyr	Leu	Glu	Ile	Val	Arg	
				395					400					405	
Glu	Asn	His	Gly	Leu	Leu	Pro	Pro	Leu	Tyr	Lys	Ser	Val	Lys	Thr	
				410					415					420	

Tyr Thr Val

<210> 242  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 242  
 catttcotta ccctggaccc agctcc 26  
  
 <210> 243  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
gaaaggccca cagcacatct ggcag 25

<210> 244  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 244  
ccacgacccg agcaacttcc tcaagaccga cttgtttctc tacagc 46

<210> 245  
<211> 485  
<212> DNA  
<213> Homo sapiens

<400> 245  
gctcaagacc cagcagtggg acagccagac agacggcacg atggcactga 50  
gctcccagat ctgggccgct tgcctcctgc tctctctct cctcgccagc 100  
ctgaccagtg gctctgtttt ccacacaacag acgggacaac ttgcagagct 150  
gcaaccccag gacagagctg gagccagggc cagctggatg cccatgttcc 200  
agaggcgaag gaggcgagac acccacttcc ccattctgcat tttctgctgc 250  
ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct 300  
acctgccctg cccccgtccc ctcccttctt tattttattcc tgctgcccc 350  
gaacataggt cttggaataa aatggctggt tcttttgttt tccccaaaaa 400  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 485

<210> 246  
<211> 84  
<212> PRT  
<213> Homo sapiens

<400> 246  
Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu  
1 5 10 15  
Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln  
20 25 30  
Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala  
35 40 45  
Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp  
50 55 60  
Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg  
65 70 75

Ser Lys Cys Gly Met Cys Cys Lys Thr

80

<210> 247

<211> 2359

<212> DNA

<213> Homo sapiens

<400> 247

ctgtcaggaa ggaccatctg aaggctgcaa tttgttctta gggaggcagg 50  
tgctggcctg gcctggatct tccaccatgt tcctgttgct gccttttgat 100  
agcctgattg tcaacctttct gggcatctcc ctgactgtcc tcttcaccct 150  
ccttctcggt ttcatcatag tgccagccat ttttgagtc tcctttggta 200  
tccgcaaaact ctacatgaaa agtctgttaa aaatctttgc gtgggctacc 250  
ttgagaatgg agcgaggagc caaggagaag aaccaccagc ttacaagcc 300  
ctacaccaac ggaatcattg caaaggatcc cacttcacta gaagaagaga 350  
tcaaagagat tcgtcgaagt ggtagtagta aggctctgga caaactcca 400  
gagttcgagc tctctgacat tttctacttt tgccggaaaag gaatggagac 450  
cattatggat gatgaggatg caaagagatt ctgagcagaa gaactggagt 500  
cctggaacct gctgagcaga accaattata acttcagta catcagcctt 550  
cggctcacgg tcctgtgggg gttaggagtg ctgattcggg actgctttct 600  
gctgccgctc aggatagcac tggctttcac agggattagc cttctgggtg 650  
tgggcacaac tgtggtggga tacttgccaa atgggaggtt taaggaattc 700  
atgagtaaac atgttcactt aatgtgttac cggatctgag tgcgagcgt 750  
gacagccatc atcacctacc atgacaggga aaacagacca agaatggtg 800  
gcatctgtgt ggccaatcat acctcacga tcgatgtgat catcttggcc 850  
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tgtgattcag agagccatgg tgaaggcctg cccacacgtc tggtttgagc 950  
gctcggaagt gaaggatgc cactggtgg ctaagagact gactgaacat 1000  
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catcaataat acatcgggtg tgatgttcaa aaagggaagt tttgaaattg 1100  
gagccacagt ttacctgtt gctatcaagt atgacctca atttggcgat 1150  
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gatgaccagc tgggccattg tctgcagcgt gtggtacctg cctcccatga 1250  
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gaagagggag aaggtgaagg acacgttcaa ggaggagcag cagaagctgt 1400  
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 cgggatccct gtgcaccggc cgcagcctac cttgtgtggt ctaaaccgat 1650  
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 cgggtacaaga gtctgttatg caagcccggtg tgccagggat gtgctggggg 1850  
 cggccacccg ctctccagga aaggcacagc tgaggcactg tggctggctt 1900  
 cggcctcaac atcgccccca gccttgagc tctgcagaca tgataggaag 1950  
 gaaactgtca tctgcagggg ctttcagcaa aatgaagggt tagattttta 2000  
 tgctgctgct gatgggggta ctaaaggag gggaagaggc cagggtgggcc 2050  
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 aactccccat gtgatgcgcg ctttgttgaa tgtgtgtctc gggtttcccca 2150  
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 tgtttcaagt acaggccac aaaacggggc acggcaggcc tgagctcaga 2300  
 gctgctgcac tgggctttgg atttgttctt gtgagtaaataaaaactggct 2350  
 ggtgaatga 2359

<210> 248

<211> 456

<212> PRT

<213> Homo sapiens

<400> 248

Met	Phe	Leu	Leu	Leu	Pro	Phe	Asp	Ser	Leu	Ile	Val	Asn	Leu	Leu
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Gly	Ile	Ser	Leu	Thr	Val	Leu	Phe	Thr	Leu	Leu	Leu	Val	Phe	Ile
				20					25					30
Ile	Val	Pro	Ala	Ile	Phe	Gly	Val	Ser	Phe	Gly	Ile	Arg	Lys	Leu
				35					40					45
Tyr	Met	Lys	Ser	Leu	Leu	Lys	Ile	Phe	Ala	Trp	Ala	Thr	Leu	Arg
				50					55					60
Met	Glu	Arg	Gly	Ala	Lys	Glu	Lys	Asn	His	Gln	Leu	Tyr	Lys	Pro
				65					70					75

Tyr	Thr	Asn	Gly	Ile	Ile	Ala	Lys	Asp	Pro	Thr	Ser	Leu	Glu	Glu	80	85	90
Glu	Ile	Lys	Glu	Ile	Arg	Arg	Ser	Gly	Ser	Ser	Lys	Ala	Leu	Asp	95	100	105
Asn	Thr	Pro	Glu	Phe	Glu	Leu	Ser	Asp	Ile	Phe	Tyr	Phe	Cys	Arg	110	115	120
Lys	Gly	Met	Glu	Thr	Ile	Met	Asp	Asp	Glu	Val	Thr	Lys	Arg	Phe	125	130	135
Ser	Ala	Glu	Glu	Leu	Glu	Ser	Trp	Asn	Leu	Leu	Ser	Arg	Thr	Asn	140	145	150
Tyr	Asn	Phe	Gln	Tyr	Ile	Ser	Leu	Arg	Leu	Thr	Val	Leu	Trp	Gly	155	160	165
Leu	Gly	Val	Leu	Ile	Arg	Tyr	Cys	Phe	Leu	Leu	Pro	Leu	Arg	Ile	170	175	180
Ala	Leu	Ala	Phe	Thr	Gly	Ile	Ser	Leu	Leu	Val	Val	Gly	Thr	Thr	185	190	195
Val	Val	Gly	Tyr	Leu	Pro	Asn	Gly	Arg	Phe	Lys	Glu	Phe	Met	Ser	200	205	210
Lys	His	Val	His	Leu	Met	Cys	Tyr	Arg	Ile	Cys	Val	Arg	Ala	Leu	215	220	225
Thr	Ala	Ile	Ile	Thr	Tyr	His	Asp	Arg	Glu	Asn	Arg	Pro	Arg	Asn	230	235	240
Gly	Gly	Ile	Cys	Val	Ala	Asn	His	Thr	Ser	Pro	Ile	Asp	Val	Ile	245	250	255
Ile	Leu	Ala	Ser	Asp	Gly	Tyr	Tyr	Ala	Met	Val	Gly	Gln	Val	His	260	265	270
Gly	Gly	Leu	Met	Gly	Val	Ile	Gln	Arg	Ala	Met	Val	Lys	Ala	Cys	275	280	285
Pro	His	Val	Trp	Phe	Glu	Arg	Ser	Glu	Val	Lys	Asp	Arg	His	Leu	290	295	300
Val	Ala	Lys	Arg	Leu	Thr	Glu	His	Val	Gln	Asp	Lys	Ser	Lys	Leu	305	310	315
Pro	Ile	Leu	Ile	Phe	Pro	Glu	Gly	Thr	Cys	Ile	Asn	Asn	Thr	Ser	320	325	330
Val	Met	Met	Phe	Lys	Lys	Gly	Ser	Phe	Glu	Ile	Gly	Ala	Thr	Val	335	340	345
Tyr	Pro	Val	Ala	Ile	Lys	Tyr	Asp	Pro	Gln	Phe	Gly	Asp	Ala	Phe	350	355	360
Trp	Asn	Ser	Ser	Lys	Tyr	Gly	Met	Val	Thr	Tyr	Leu	Leu	Arg	Met	365	370	375
Met	Thr	Ser	Trp	Ala	Ile	Val	Cys	Ser	Val	Trp	Tyr	Leu	Pro	Pro	380	385	390

Met	Thr	Arg	Glu	Ala	Asp	Glu	Asp	Ala	Val	Gln	Phe	Ala	Asn	Arg
				395					400					405
Val	Lys	Ser	Ala	Ile	Ala	Arg	Gln	Gly	Gly	Leu	Val	Asp	Leu	Leu
				410					415					420
Trp	Asp	Gly	Gly	Leu	Lys	Arg	Glu	Lys	Val	Lys	Asp	Thr	Phe	Lys
				425					430					435
Glu	Glu	Gln	Gln	Lys	Leu	Tyr	Ser	Lys	Met	Ile	Val	Gly	Asn	His
				440					445					450
Lys	Asp	Arg	Ser	Arg	Ser									
				455										

<210> 249  
 <211> 1103  
 <212> DNA  
 <213> Homo sapiens

<400> 249  
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 gccctcggca gcctcggcct ccacacctgg caggcccagg ctgttcccac 150  
 catcctgccc ctgggcctgg ctccagacac ctttgacgat acctatgtgg 200  
 gttgtgcaga ggagatggag gagaaggcag cccccctgct aaaggaggaa 250  
 atggcccacc atgccttgcct gcgggaatcc tgggaggcag ccaggagac 300  
 ctgggaggac aagcgtcgag ggcttacctt gccccctggc ttcaaagccc 350  
 agaatggaat agccattatg gtctacacca actcatogaa caccttgtac 400  
 tgggagttga atcaggccgt gcggacgggc ggaggctccc gggagctcta 450  
 catgaggcac tttcccttca aggcctgca tttctacctg atccgggccc 500  
 tgcagctgct gcgaggcagt gggggctgca gcaggggacc tggggaggtg 550  
 gtgttccgag gtgtgggcag ccttcgcttt gaacccaaga ggctggggga 600  
 ctctgtccgc ttgggccagt ttgcctccag ctccctggat aaggcagtgg 650  
 cccacagatt tggggagaag aggcggggct gtgtgtctgc gccaggggtg 700  
 cagctagggt cacaatctga gggggcctcc tctctgcccc cctggaagac 750  
 tctgtctttg gccctggag agttccagct ctccaggggtt gggccctgaa 800  
 agtccaacat ctgccactta ggagccctgg gaacgggtga ccttcatatg 850  
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 ccagccctag cagccttctc cccaaccagg atgttggcct ggggaggcca 950  
 cagcagggct gagggaaact tgctatgtga tggggacttc ctgggacaag 1000  
 caaggaaagt actgaggcag ccacttgatt gaacggtgtt gcaatgtgga 1050

gacatggagt tttattgagg tagctacgtg attaaatggt attgcagtgt 1100

gga 1103

<210> 250

<211> 240

<212> PRT

<213> Homo sapiens

<400> 250

Met Ala Leu Ala Ala Leu Met Ile Ala Leu Gly Ser Leu Gly Leu  
1 5 10 15

His Thr Trp Gln Ala Gln Ala Val Pro Thr Ile Leu Pro Leu Gly  
20 25 30

Leu Ala Pro Asp Thr Phe Asp Asp Thr Tyr Val Gly Cys Ala Glu  
35 40 45

Glu Met Glu Glu Lys Ala Ala Pro Leu Leu Lys Glu Glu Met Ala  
50 55 60

His His Ala Leu Leu Arg Glu Ser Trp Glu Ala Ala Gln Glu Thr  
65 70 75

Trp Glu Asp Lys Arg Arg Gly Leu Thr Leu Pro Pro Gly Phe Lys  
80 85 90

Ala Gln Asn Gly Ile Ala Ile Met Val Tyr Thr Asn Ser Ser Asn  
95 100 105

Thr Leu Tyr Trp Glu Leu Asn Gln Ala Val Arg Thr Gly Gly Gly  
110 115 120

Ser Arg Glu Leu Tyr Met Arg His Phe Pro Phe Lys Ala Leu His  
125 130 135

Phe Tyr Leu Ile Arg Ala Leu Gln Leu Leu Arg Gly Ser Gly Gly  
140 145 150

Cys Ser Arg Gly Pro Gly Glu Val Val Phe Arg Gly Val Gly Ser  
155 160 165

Leu Arg Phe Glu Pro Lys Arg Leu Gly Asp Ser Val Arg Leu Gly  
170 175 180

Gln Phe Ala Ser Ser Ser Leu Asp Lys Ala Val Ala His Arg Phe  
185 190 195

Gly Glu Lys Arg Arg Gly Cys Val Ser Ala Pro Gly Val Gln Leu  
200 205 210

Gly Ser Gln Ser Glu Gly Ala Ser Ser Leu Pro Pro Trp Lys Thr  
215 220 225

Leu Leu Leu Ala Pro Gly Glu Phe Gln Leu Ser Gly Val Gly Pro  
230 235 240

<210> 251

<211> 50

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
ccaccacctg gaggtcctgc agttgggcag gaactccatc cggcagattg 50

<210> 252

<211> 1076

<212> DNA

<213> Homo sapiens

<400> 252  
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caacatgcct caccctcatc tatatccttt ggcagctcac agggtcagca 100  
gcctctggac ccgtgaaaga gctggtcggt tccgttggtg gggccgtgac 150  
tttccccctg aagtccaaag taaagcaagt tgactctatt gtctggacct 200  
tcaacacaac ccctcttgtc accatacagc cagaaggggg cactatcata 250  
gtgacccaaa atcgtaatag ggagagagta gacttcccag atggaggcta 300  
ctccctgaag ctacagcaaac tgaagaagaa tgactcaggg atctactatg 350  
tggggatata cagctcatca ctccagcagc cctccaccca ggagtacgtg 400  
ctgcatgtct acgagcacct gtcaaagcct aaagtcacca tgggtctgca 450  
gagcaataag aatggcacct gtgtgaccaa tctgacatgc tgcattggaac 500  
atggggaaga ggatgtgatt tatacctgga aggccctggg gcaagcagcc 550  
aatgagtcct ataattgggtc catcctcccc atctcctgga gatggggaga 600  
aagtgatatg accttcatct gcgttgccag gaacctgtc agcagaaaact 650  
tctcaagccc catccttgcc aggaagctct gtgaagggtc tgctgatgac 700  
ccagattcct ccattggtcct cctgtgtctc ctgttggtgc cctcctgct 750  
cagtctcttt gtactggggc tatttctttg gtttctgaag agagagagac 800  
aagaagagta cattgaagag aagaagagag tggacatttg tcgggaaact 850  
cctaacatat gccccattc tggagagaac acagagtacg acacaatccc 900  
tcacactaat agaacaatcc taaaggaaga tccagcaaat acggtttact 950  
ccactgtgga aataccgaaa aagatggaaa atcccactc actgctcacg 1000  
atgccagaca caccaaggct atttgcctat gagaatgtta tctagacagc 1050  
agtgcactcc cctaagtctc tgetca 1076

<210> 253

<211> 335

<212> PRT

<213> Homo sapiens

<400> 253

Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp

1	5	10	15
Gln Leu Thr Gly Ser	Ala Ala Ser Gly	Pro Val Lys Glu Leu Val	
	20	25	30
Gly Ser Val Gly Gly	Ala Val Thr Phe	Pro Leu Lys Ser Lys Val	
	35	40	45
Lys Gln Val Asp Ser	Ile Val Trp Thr	Phe Asn Thr Thr Pro Leu	
	50	55	60
Val Thr Ile Gln Pro	Glu Gly Gly Thr	Ile Ile Val Thr Gln Asn	
	65	70	75
Arg Asn Arg Glu Arg	Val Asp Phe Pro	Asp Gly Gly Tyr Ser Leu	
	80	85	90
Lys Leu Ser Lys Leu	Lys Lys Asn Asp	Ser Gly Ile Tyr Tyr Val	
	95	100	105
Gly Ile Tyr Ser Ser	Ser Leu Gln Gln	Pro Ser Thr Gln Glu Tyr	
	110	115	120
Val Leu His Val Tyr	Glu His Leu Ser	Lys Pro Lys Val Thr Met	
	125	130	135
Gly Leu Gln Ser Asn	Lys Asn Gly Thr	Cys Val Thr Asn Leu Thr	
	140	145	150
Cys Cys Met Glu His	Gly Glu Glu Asp	Val Ile Tyr Thr Trp Lys	
	155	160	165
Ala Leu Gly Gln Ala	Ala Asn Glu Ser	His Asn Gly Ser Ile Leu	
	170	175	180
Pro Ile Ser Trp Arg	Trp Gly Glu Ser	Asp Met Thr Phe Ile Cys	
	185	190	195
Val Ala Arg Asn Pro	Val Ser Arg Asn	Phe Ser Ser Pro Ile Leu	
	200	205	210
Ala Arg Lys Leu Cys	Glu Gly Ala Ala	Asp Asp Pro Asp Ser Ser	
	215	220	225
Met Val Leu Leu Cys	Leu Leu Leu Val	Pro Leu Leu Leu Ser Leu	
	230	235	240
Phe Val Leu Gly Leu	Phe Leu Trp Phe	Leu Lys Arg Glu Arg Gln	
	245	250	255
Glu Glu Tyr Ile Glu	Glu Lys Lys Arg	Val Asp Ile Cys Arg Glu	
	260	265	270
Thr Pro Asn Ile Cys	Pro His Ser Gly	Glu Asn Thr Glu Tyr Asp	
	275	280	285
Thr Ile Pro His Thr	Asn Arg Thr Ile	Leu Lys Glu Asp Pro Ala	
	290	295	300
Asn Thr Val Tyr Ser	Thr Val Glu Ile	Pro Lys Lys Met Glu Asn	
	305	310	315
Pro His Ser Leu Leu	Thr Met Pro Asp	Thr Pro Arg Leu Phe Ala	

320

325

330

Tyr Glu Asn Val Ile  
335

<210> 254  
<211> 1053  
<212> DNA  
<213> Homo sapiens

<400> 254  
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gggtcagcag cctctggacc cgtgaaagag ctggtcggtt ccgttgggtg 100  
ggcctgact ttccccctga agtccaaagt aaagcaagtt gactctattg 150  
tctggacctt caacacaacc cctcttgtca ccatacagcc agaagggggc 200  
actatcatag tgacccaaaa tcgtaatagg gagagagtag acttcccaga 250  
tggaggctac tccctgaagc tcagcaaaact gaagaagaat gactcaggga 300  
tctactatgt ggggatatac agctcatcac tccagcagcc ctccaccag 350  
gagtacgtgc tgcattgtcta cgagcacctg tcaaagccta aagtcaccat 400  
gggtctgcag agcaataaga atggcacctg tgtgaccaat ctgacatgct 450  
gcatggaaca tggggaagag gatgtgattt atacctggaa ggcctgggg 500  
caagcagcca atgagtccca taatgggtcc atcctcccca tctcctggag 550  
atggggagaa agtgatatga ccttcatctg cgttgccagg aaccctgtca 600  
gcagaaactt ctcaagcccc atccttgcca ggaagctctg tgaaggtgct 650  
gctgatgacc cagattcctc catggctcctc ctgtgtctcc tgttgggtgcc 700  
cctcctgctc agtctctttg tactgggggt atttctttgg tttctgaaga 750  
gagagagaca agaagagtac attgaagaga agaagagagt ggacatttgt 800  
cgggaaactc ctaacatatg cccccattct ggagagaaca cagagtacga 850  
cacaatccct cacactaata gaacaatcct aaaggaagat ccagcaaata 900  
cgttttactc cactgtggaa ataccgaaaa agatggaaaa tccccactca 950  
ctgctcacga tgccagacac accaaggcta tttgcctatg agaatgttat 1000  
ctagacagca gtgcactccc ctaagtctct gctcaaaaaa aaaaaaaaaa 1050  
aaa 1053

<210> 255  
<211> 860  
<212> DNA  
<213> Homo sapiens

<400> 255  
gaaagacgtg gtcctgacag acagacaatc ctattcccta ccaaaatgaa 50

gatgctgctg ctgctgtggt tgggactgac cctagtctgt gtccatgcag 100  
aagaagctag ttctacggga aggaacttta atgtagaaaa gattaatggg 150  
gaatggcata ctattatcct ggcctctgac aaaagagaaa agatagaaga 200  
acatggcaac tttagacttt ttctggagca aatccatgtc ttggagaatt 250  
ccttagttct taaagtccat actgtaagag atgaagagtg ctccgaatta 300  
tctatgggtg ctgacaaaac agaaaaggct ggtgaatatt ctgtgacgta 350  
tgatggattc aatacattta ctatacctaa gacagactat gataactttc 400  
ttatggctca cctcattaac gaaaaggatg gggaaacctt ccagctgatg 450  
gggctctatg gccgagaacc agatttgagt tcagacatca aggaaagggt 500  
tgcacaacta tgtgaggagc atggaatcct tagagaaaat atcattgacc 550  
tatccaatgc caatcgctgc ctccaggccc gagaatgaag aatggcctga 600  
gcctccagtg ttgagtggac acttctcacc aggactccac catcatccct 650  
tcctatccat acagcatccc cagtataaat tctgtgatct gcattccatc 700  
ctgtctcact gagaagtcca attccagtct atcaacatgt tacctaggat 750  
acctcatcaa gaatcaaaga cttctttaaa tttctctttg atacaccctt 800  
gacaattttt catgaaatta ttctcttcc tgttcaataa atgattaccc 850  
ttgcacttaa 860

<210> 256  
<211> 180  
<212> PRT  
<213> Homo sapiens

<400> 256  
Met Lys Met Leu Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys  
1 5 10 15  
Val His Ala Glu Glu Ala Ser Ser Thr Gly Arg Asn Phe Asn Val  
20 25 30  
Glu Lys Ile Asn Gly Glu Trp His Thr Ile Ile Leu Ala Ser Asp  
35 40 45  
Lys Arg Glu Lys Ile Glu Glu His Gly Asn Phe Arg Leu Phe Leu  
50 55 60  
Glu Gln Ile His Val Leu Glu Asn Ser Leu Val Leu Lys Val His  
65 70 75  
Thr Val Arg Asp Glu Glu Cys Ser Glu Leu Ser Met Val Ala Asp  
80 85 90  
Lys Thr Glu Lys Ala Gly Glu Tyr Ser Val Thr Tyr Asp Gly Phe  
95 100 105  
Asn Thr Phe Thr Ile Pro Lys Thr Asp Tyr Asp Asn Phe Leu Met  
110 115 120

Ala	His	Leu	Ile	Asn	Glu	Lys	Asp	Gly	Glu	Thr	Phe	Gln	Leu	Met
				125					130					135
Gly	Leu	Tyr	Gly	Arg	Glu	Pro	Asp	Leu	Ser	Ser	Asp	Ile	Lys	Glu
				140					145					150
Arg	Phe	Ala	Gln	Leu	Cys	Glu	Glu	His	Gly	Ile	Leu	Arg	Glu	Asn
				155					160					165
Ile	Ile	Asp	Leu	Ser	Asn	Ala	Asn	Arg	Cys	Leu	Gln	Ala	Arg	Glu
				170					175					180

<210> 257  
 <211> 766  
 <212> DNA  
 <213> Homo sapiens

<400> 257  
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 gacatcctgc aatggattca gcctgctggt tctactgctg ttaggagtag 100  
 ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaatth 150  
 tctcaaaacc ccattctctg ctttgagtgg tggttoccag gaattatagg 200  
 agcagggtctg atggccattc cagcaacaac aatgtccttg acagcaagaa 250  
 aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc 300  
 agtgtgatca cagtcattgg tgctctgtat tgcattgctga tatccatcca 350  
 ggctctctta aaaggctctc tcatgtgtaa ttctccaagc aacagtaatg 400  
 ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450  
 ttcaacttgc agtggttttt caatgactot tgtgcacctc ctactggttt 500  
 caataaacc accagtaacg acaccatggc gagtggctgg agagcatcta 550  
 gtttccactt cgattctgaa gaaaacaaac ataggcttat ccactttctca 600  
 gtatttttag gtctattgct tgttggaatt ctggagggtcc tgtttgggct 650  
 cagtcagata gtcacggtt tcttggtgctg tctgtgtgga gtctctaagc 700  
 gaagaagtca aattgtgtag tttaattggga ataaatgta agtatcagta 750  
 gtttgaaaaa aaaaaa 766

<210> 258  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 258  
 Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu  
 1 5 10 15  
 Leu Val Leu Leu Leu Gly Val Val Leu Asn Ala Ile Pro Leu  
 20 25 30  
 Ile Val Ser Leu Val Glu Glu Asp Gln Phe Ser Gln Asn Pro Ile

35					40					45				
Ser	Cys	Phe	Glu	Trp	Trp	Phe	Pro	Gly	Ile	Ile	Gly	Ala	Gly	Leu
			50						55					60
Met	Ala	Ile	Pro	Ala	Thr	Thr	Met	Ser	Leu	Thr	Ala	Arg	Lys	Arg
			65						70					75
Ala	Cys	Cys	Asn	Asn	Arg	Thr	Gly	Met	Phe	Leu	Ser	Ser	Phe	Phe
			80						85					90
Ser	Val	Ile	Thr	Val	Ile	Gly	Ala	Leu	Tyr	Cys	Met	Leu	Ile	Ser
			95						100					105
Ile	Gln	Ala	Leu	Leu	Lys	Gly	Pro	Leu	Met	Cys	Asn	Ser	Pro	Ser
			110						115					120
Asn	Ser	Asn	Ala	Asn	Cys	Glu	Phe	Ser	Leu	Lys	Asn	Ile	Ser	Asp
			125						130					135
Ile	His	Pro	Glu	Ser	Phe	Asn	Leu	Gln	Trp	Phe	Phe	Asn	Asp	Ser
			140						145					150
Cys	Ala	Pro	Pro	Thr	Gly	Phe	Asn	Lys	Pro	Thr	Ser	Asn	Asp	Thr
			155						160					165
Met	Ala	Ser	Gly	Trp	Arg	Ala	Ser	Ser	Phe	His	Phe	Asp	Ser	Glu
			170						175					180
Glu	Asn	Lys	His	Arg	Leu	Ile	His	Phe	Ser	Val	Phe	Leu	Gly	Leu
			185						190					195
Leu	Leu	Val	Gly	Ile	Leu	Glu	Val	Leu	Phe	Gly	Leu	Ser	Gln	Ile
			200						205					210
Val	Ile	Gly	Phe	Leu	Gly	Cys	Leu	Cys	Gly	Val	Ser	Lys	Arg	Arg
			215						220					225

Ser Gln Ile Val

<210> 259  
 <211> 434  
 <212> DNA  
 <213> Homo sapiens

<400> 259  
 gtcgaatcca aatcactcat tgtgaaagct gagctcacag ccgaataagc 50  
 caccatgagg ctgtcagtgt gtctctgat ggtctcgctg gccctttgct 100  
 gctaccaggc ccatgctctt gtctgccag ctgttgcttc tgagatcaca 150  
 gtctttttat tcttaagtga cgctgcggta aacctccaag ttgccaaact 200  
 taatccacct ccagaagctc ttgcagccaa gttggaagtg aagcactgca 250  
 ccgatcagat atctttttaag aaacgactct cattgaaaaa gtcttggtgg 300  
 aaatagtga aaaaatgtgg gtgtgacatg taaaaatgct caacctggtt 350  
 tccaaagtct ttcaacgaca ccctgatctt cactaaaaat tgtaaagggtt 400

tcaacacggtt gctttaataa atcacttgcc ctgc 434

<210> 260  
<211> 83  
<212> PRT  
<213> Homo sapiens

<400> 260  
Met Arg Leu Ser Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys  
1 5 10 15  
Cys Tyr Gln Ala His Ala Leu Val Cys Pro Ala Val Ala Ser Glu  
20 25 30  
Ile Thr Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln  
35 40 45  
Val Ala Lys Leu Asn Pro Pro Pro Glu Ala Leu Ala Ala Lys Leu  
50 55 60  
Glu Val Lys His Cys Thr Asp Gln Ile Ser Phe Lys Lys Arg Leu  
65 70 75  
Ser Leu Lys Lys Ser Trp Trp Lys  
80

<210> 261  
<211> 636  
<212> DNA  
<213> Homo sapiens

<400> 261  
atccgttctc tgcgctgcc a gctcaggtga gccctcgcca aggtgacctc 50  
gcaggacact ggtgaaggag cagtgaggaa cctgcagagt cacacagttg 100  
ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc 150  
cgccccagtg cctctcccc tgcagccctg cccctogaac tgtgacatgg 200  
agagagtgc cctggccctt ctctactgg caggcctgac tgccttgga 250  
gccaatgacc catttgcaa taaagacgat ccctctact atgactggaa 300  
aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg 350  
ggatcgcggc agttctgagt ggcaaagca aatacaagag cagccagaag 400  
cagcacagtc ctgtacctga gaaggccatc ccaactcatca ctccaggctc 450  
tgccactact tgctgagcac aggactggcc tccagggatg gcctgaagcc 500  
taacactggc cccagcacc tctccctctg ggaggcctta tctcaagga 550  
aggacttctc tccaaggga ggctgttagg cccctttctg atcaggaggc 600  
ttctttatga attaaactcg cccaccacc ccctca 636

<210> 262  
<211> 89  
<212> PRT  
<213> Homo sapiens

<400> 262

Met Glu Arg Val Thr Leu Ala Leu Leu Leu Leu Ala Gly Leu Thr  
1 5 10 15

Ala Leu Glu Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe  
20 25 30

Tyr Tyr Asp Trp Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly  
35 40 45

Gly Leu Leu Ala Ile Ala Gly Ile Ala Ala Val Leu Ser Gly Lys  
50 55 60

Cys Lys Tyr Lys Ser Ser Gln Lys Gln His Ser Pro Val Pro Glu  
65 70 75

Lys Ala Ile Pro Leu Ile Thr Pro Gly Ser Ala Thr Thr Cys  
80 85

<210> 263

<211> 1676

<212> DNA

<213> Homo sapiens

<400> 263

ggagaagagg ttgtgtggga caagctgctc ccgacagaag gatgtcgtg 50

ctgagcctgc cctggctggg cctcagaccg gtggcaatgt ccccatggct 100

actcctgctg ctggttgtgg gctcctggct actcgccgc atcctggctt 150

ggacctatgc cttctataac aactgccgcc ggctccagtg tttccacag 200

ccccaaaac ggaactggtt ttggggtcac ctgggcctga tcaactctac 250

agaggagggc ttgaaggact cgaccagat gtcggccacc tattccag 300

gctttacggt atggctgggt cccatcatcc ccttcacgt tttatgccac 350

cctgacacca tccggtctat caccaatgcc tcagctgcca ttgcacccaa 400

ggataatctc ttcacaggt tctgaagcc ctggctggga gaagggatac 450

tgctgagtgg cggtgacaag tggagccgcc accgtcggat gctgacgccc 500

gccttccatt tcaacatcct gaagtcctat ataacgatct tcaacaagag 550

tgcaaacatc atgcttgaca agtggcagca cctggcctca gagggcagca 600

gtcgtctgga catgtttgag cacatcagcc tcatgacctt ggacagtcta 650

cagaaatgca tcttcagctt tgacagccat tgtcaggaga ggcccagtga 700

atatattgcc accatcttgg agctcagtg ccttgtagag aaaagaagcc 750

agcatatcct ccagcacatg gactttctgt attacctctc ccatgacggg 800

cggcgcttcc acagggcctg ccgcctgggt catgacttca cagacgctgt 850

catccgggag cggcgtcgca cctcccccac tcagggtatt gatgattttt 900

tcaaagacaa agccaagtcc aagactttgg atttcattga tgtgcttctg 950

ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc 1000  
 agaggctgac accttcatgt ttggaggcca tgacaccacg gccagtggcc 1050  
 tctcctgggt cctgtacaac cttgcgaggc acccagaata ccaggagcgc 1100  
 tgccgacagg aggtgcaaga gcttctgaag gaccgcgac ctaaagagat 1150  
 tgaatgggac gacctggccc agctgccctt cctgaccatg tgcgtgaagg 1200  
 agagcctgag gttacatccc ccagctccct tcctctcccg atgctgcacc 1250  
 caggacattg ttctcccaga tggccgagtc atccccaaag gcattacctg 1300  
 cctcatcgat attatagggg tccatcacia cccaactgtg tggccggatc 1350  
 ctgaggtcta cgaccccttc cgctttgacc cagagaacag caaggggagg 1400  
 tcacctctgg cttttattcc tttctccgca gggcccagga actgcatcgg 1450  
 gcaggcgttc gccatggcgg agatgaaagt ggtcctggcg ttgatgctgc 1500  
 tgcacttccg gttcctgcca gaccacactg agccccgcag gaagctggaa 1550  
 ttgatcatgc gcgcgagggg cgggctttgg ctgcgggtgg agcccctgaa 1600  
 tgtaggcttg cagtgaactt ctgaccatc cacctgtttt tttgcagatt 1650  
 gtcatgaata aaacgggtgct gtcaaaa 1676

<210> 264  
 <211> 524  
 <212> PRT  
 <213> Homo sapiens

<400> 264  
 Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala  
 1 5 10 15  
 Met Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu  
 20 25 30  
 Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys  
 35 40 45  
 Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe  
 50 55 60  
 Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys  
 65 70 75  
 Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val  
 80 85 90  
 Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp  
 95 100 105  
 Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys  
 110 115 120  
 Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly  
 125 130 135

Ile	Leu	Leu	Ser	Gly	Gly	Asp	Lys	Trp	Ser	Arg	His	Arg	Arg	Met	140	145	150
Leu	Thr	Pro	Ala	Phe	His	Phe	Asn	Ile	Leu	Lys	Ser	Tyr	Ile	Thr	155	160	165
Ile	Phe	Asn	Lys	Ser	Ala	Asn	Ile	Met	Leu	Asp	Lys	Trp	Gln	His	170	175	180
Leu	Ala	Ser	Glu	Gly	Ser	Ser	Arg	Leu	Asp	Met	Phe	Glu	His	Ile	185	190	195
Ser	Leu	Met	Thr	Leu	Asp	Ser	Leu	Gln	Lys	Cys	Ile	Phe	Ser	Phe	200	205	210
Asp	Ser	His	Cys	Gln	Glu	Arg	Pro	Ser	Glu	Tyr	Ile	Ala	Thr	Ile	215	220	225
Leu	Glu	Leu	Ser	Ala	Leu	Val	Glu	Lys	Arg	Ser	Gln	His	Ile	Leu	230	235	240
Gln	His	Met	Asp	Phe	Leu	Tyr	Tyr	Leu	Ser	His	Asp	Gly	Arg	Arg	245	250	255
Phe	His	Arg	Ala	Cys	Arg	Leu	Val	His	Asp	Phe	Thr	Asp	Ala	Val	260	265	270
Ile	Arg	Glu	Arg	Arg	Arg	Thr	Leu	Pro	Thr	Gln	Gly	Ile	Asp	Asp	275	280	285
Phe	Phe	Lys	Asp	Lys	Ala	Lys	Ser	Lys	Thr	Leu	Asp	Phe	Ile	Asp	290	295	300
Val	Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Gly	Lys	Ala	Leu	Ser	Asp	305	310	315
Glu	Asp	Ile	Arg	Ala	Glu	Ala	Asp	Thr	Phe	Met	Phe	Gly	Gly	His	320	325	330
Asp	Thr	Thr	Ala	Ser	Gly	Leu	Ser	Trp	Val	Leu	Tyr	Asn	Leu	Ala	335	340	345
Arg	His	Pro	Glu	Tyr	Gln	Glu	Arg	Cys	Arg	Gln	Glu	Val	Gln	Glu	350	355	360
Leu	Leu	Lys	Asp	Arg	Asp	Pro	Lys	Glu	Ile	Glu	Trp	Asp	Asp	Leu	365	370	375
Ala	Gln	Leu	Pro	Phe	Leu	Thr	Met	Cys	Val	Lys	Glu	Ser	Leu	Arg	380	385	390
Leu	His	Pro	Pro	Ala	Pro	Phe	Ile	Ser	Arg	Cys	Cys	Thr	Gln	Asp	395	400	405
Ile	Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Pro	Lys	Gly	Ile	Thr	Cys	410	415	420
Leu	Ile	Asp	Ile	Ile	Gly	Val	His	His	Asn	Pro	Thr	Val	Trp	Pro	425	430	435
Asp	Pro	Glu	Val	Tyr	Asp	Pro	Phe	Arg	Phe	Asp	Pro	Glu	Asn	Ser	440	445	450

Lys	Gly	Arg	Ser	Pro	Leu	Ala	Phe	Ile	Pro	Phe	Ser	Ala	Gly	Pro
				455					460					465
Arg	Asn	Cys	Ile	Gly	Gln	Ala	Phe	Ala	Met	Ala	Glu	Met	Lys	Val
				470					475					480
Val	Leu	Ala	Leu	Met	Leu	Leu	His	Phe	Arg	Phe	Leu	Pro	Asp	His
				485					490					495
Thr	Glu	Pro	Arg	Arg	Lys	Leu	Glu	Leu	Ile	Met	Arg	Ala	Glu	Gly
				500					505					510
Gly	Leu	Trp	Leu	Arg	Val	Glu	Pro	Leu	Asn	Val	Gly	Leu	Gln	
				515					520					

<210> 265  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens

<400> 265  
 caacagaagc caagaaggaa gccgtctatc ttgtggcgat catgtataag 50  
 ctggcctcct gctgtttgct ttccacagga ttcttaaata ctctcttata 100  
 tcttcctctc cttgactcca gggaaatata ctttcaactc tcagcacctc 150  
 atgaagaagc gcgcttaact cggaggagc tagaaagagc ttcccttcta 200  
 cagatattgc cagagatgct ggggtgcagaa agaggggata ttctcaggaa 250  
 agcagactca agtaccaaca tttttaaccc aagaggaaat ttgagaaagt 300  
 ttcaggattt ctctggacaa gacctaaca ttttactgag tcattcttttg 350  
 gccagaatct ggaaaccata caagaaacgt gagactcctg attgcttctg 400  
 gaaatactgt gtctgaagtg aaataagcat ctgttagtca gtcagaaac 450  
 acccatctta gaatatgaaa aataacacaa tgcttgattt gaaaacagtg 500  
 tggagaaaaa ctaggcaaac tacacctgt tcattgttac ctggaaaata 550  
 aatcctctat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 266  
 Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Thr Gly Phe Leu  
 1 5 10 15  
 Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser  
 20 25 30  
 Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu  
 35 40 45  
 Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu  
 50 55 60

Gly	Ala	Glu	Arg	Gly	Asp	Ile	Leu	Arg	Lys	Ala	Asp	Ser	Ser	Thr
				65					70					75
Asn	Ile	Phe	Asn	Pro	Arg	Gly	Asn	Leu	Arg	Lys	Phe	Gln	Asp	Phe
				80					85					90
Ser	Gly	Gln	Asp	Pro	Asn	Ile	Leu	Leu	Ser	His	Leu	Leu	Ala	Arg
				95					100					105
Ile	Trp	Lys	Pro	Tyr	Lys	Lys	Arg	Glu	Thr	Pro	Asp	Cys	Phe	Trp
				110					115					120

Lys Tyr Cys Val

<210> 267  
 <211> 654  
 <212> DNA  
 <213> Homo sapiens

<400> 267  
 gaacattttt agttcccaag gaatgtacat cagccccacg gaagctaggc 50  
 cacctctggg atgggggttg tggtttaaaa caaacgccag tcatcctata 100  
 taaggacctg acagccacca ggcaccacct ccgccaggaa ctgcaggccc 150  
 acctgtctgc aaccagctg aggccatgcc ctcccaggga accgtctgca 200  
 gcctcctgct cctcggcatg ctctggctgg acttggccat ggcaggctcc 250  
 agcttcctga gccctgaaca ccagagagtc cagcagagaa aggagtcgaa 300  
 gaagccacca gccaaagtgc agccccgagc tctagcaggc tggctccgcc 350  
 cggaagatgg aggtcaagca gaaggggcag aggatgaact ggaagtccgg 400  
 ttcaacgccc cttttgatgt tggaatcaag ctgtcagggg ttcagtacca 450  
 gcagcacagc caggccctgg ggaagtttct tcaggacatc ctctgggaag 500  
 aggccaaaga ggccccagcc gacaagtgat cgcacacaag ccttactcac 550  
 ctctctctaa gtttagaagc gctcatctgg cttttcgctt gcttctgcag 600  
 caactcccac gactgttgta caagctcagg aggcgaataa atgttcaaac 650  
 tgta 654

<210> 268  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 268  
 Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met  
 1 5 10 15  
 Leu Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro  
 20 25 30  
 Glu His Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro  
 35 40 45

Ala	Lys	Leu	Gln	Pro	Arg	Ala	Leu	Ala	Gly	Trp	Leu	Arg	Pro	Glu
				50					55					60
Asp	Gly	Gly	Gln	Ala	Glu	Gly	Ala	Glu	Asp	Glu	Leu	Glu	Val	Arg
			65						70					75
Phe	Asn	Ala	Pro	Phe	Asp	Val	Gly	Ile	Lys	Leu	Ser	Gly	Val	Gln
			80						85					90
Tyr	Gln	Gln	His	Ser	Gln	Ala	Leu	Gly	Lys	Phe	Leu	Gln	Asp	Ile
			95						100					105
Leu	Trp	Glu	Glu	Ala	Lys	Glu	Ala	Pro	Ala	Asp	Lys			
			110						115					

<210> 269  
 <211> 1332  
 <212> DNA  
 <213> Homo sapiens

<400> 269  
 cggccacagc tggcatgctc tgccatgatcg ccacccctgct gtatgtcctc 50  
 gtccagtagc tcgtgaaccc cgggggtgctc cgcacggacc ccagatgtca 100  
 agaatatgaa cacgtggctg ctgttcctcc cctgtttccc ggtgcagggtg 150  
 cagaccctga tagtcgtgat catcgggatg ctgtgtctcc tgctggactt 200  
 tcttggtctg gtgcacctgg gccagctgct catcttccac atctacctga 250  
 gtatgtcccc caccctaagc ccccgatccc cccaaggctg ggtggtcaga 300  
 gctgtctcatc ttacacctct acttgagtat gtccctaacc ctgagccccc 350  
 cacgcctggg gccagagtct ttgtcccccg tgtgcgcatg tgttcagggt 400  
 cagcctctcc cagaagttag atcatggaca aaaagggaac atcacaggaa 450  
 gaaattaaat ccatgaggac ccagcaggcc cagcaagaag ctgaactcac 500  
 gccgagacct gcaggagtgg tgccagggtg ttgaagtaac aagtttaaaa 550  
 tgttcagaga caatggaatg gaatctatta ggcaagaaca ggacattatg 600  
 aaataaggac aggtggactt ccaaaaacac aagtagaat tctaacaatg 650  
 aaatatatta caggcaggtc acccactaac caaacaaactg aagcgagagc 700  
 tgtggtcttg cttggtctca cagtgggcac agcggtaggc ggtcagtcac 750  
 gttgtctgac gacggagggt aaactcccca gccccaagaa aacctgtgtt 800  
 ggaagtaaca acaacctccc tgcctctggc accagccgtt ttggtcatgg 850  
 tgggccagct gcaaagcgtc ttccattctc tgggcagtgg tggccccgag 900  
 gctgtggcct ctcagggggg ttctgtggac acgggcagca gactgtgtcc 950  
 aggccagccc ccaagaatgc cctgctcctg acagcttggc caaccctgg 1000  
 tcagggcaga gggagttggg tgggtcaggc tctgggctca cctccatctc 1050

cagagcatcc cctgcctgca gttgtggcaa gaacgccag ctcagaatga 1100  
acacacccca ccaagagcct ccttgttcat aaccacaggt taccctacaa 1150  
accactgtcc ccacacaacc ctggggatgt tttaaaacac acacctctaa 1200  
cgcatatctt acagtcactg ttgtcttgcc tgaggggtga atttttttta 1250  
atgaaagtgc aatgaaaatc actggattaa atcctacgga cacagagctg 1300  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1332

<210> 270  
<211> 142  
<212> PRT  
<213> Homo sapiens

<400> 270  
Met Asn Thr Trp Leu Leu Phe Leu Pro Leu Phe Pro Val Gln Val  
1 5 10 15  
Gln Thr Leu Ile Val Val Ile Ile Gly Met Leu Val Leu Leu Leu  
20 25 30  
Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu Leu Ile Phe His  
35 40 45  
Ile Tyr Leu Ser Met Ser Pro Thr Leu Ser Pro Arg Ser Pro Gln  
50 55 60  
Gly Trp Val Val Arg Ala Ala His Leu Thr Pro Leu Leu Glu Tyr  
65 70 75  
Val Pro Asn Pro Glu Pro Pro Thr Pro Gly Ala Arg Val Phe Val  
80 85 90  
Pro Arg Val Arg Met Cys Ser Gly Ser Ala Ser Pro Arg Ser Glu  
95 100 105  
Ile Met Asp Lys Lys Gly Lys Ser Gln Glu Glu Ile Lys Ser Met  
110 115 120  
Arg Thr Gln Gln Ala Gln Gln Glu Ala Glu Leu Thr Pro Arg Pro  
125 130 135  
Ala Gly Val Val Pro Gly Ala  
140

<210> 271  
<211> 1484  
<212> DNA  
<213> Homo sapiens

<400> 271  
ggagtgcaga tggcatcctt cggttcttcc agacaagctg caagacgctg 50  
accatggcca agatggagct ctgaaggcc ttctctggcc agcggacact 100  
cctatctgcc atcctcagca tgctatcact cagcttctcc acaacatccc 150  
tgctcagcaa ctactggttt gtgggcacac agaaggtgcc caagcccctg 200  
tgcgagaaag gtctggcagc caagtgcctt gacatgccag tgtccctgga 250

tggagatacc aacacatcca cccaggaggt ggtacaatac aactgggaga 300  
 ctggggatga ccggttctcc ttccggagct tccggagtgg catgtggcta 350  
 tctgttgagg aaactgtgga agaaccaggg gagaggtgcc gaagtttcat 400  
 tgaacttaca ccaccagcca agagaggtga gaaaggacta ctggaatttg 450  
 ccacgttgca aggcccatgt caccctactc tccgatttgg agggaagcgg 500  
 ttgatggaga aggccttccct cccctcccct cccttggggc tttgtggcaa 550  
 aaatcctatg gttatccctg ggaacgcaga tcacctacat cggacttcaa 600  
 ttcatcagct tcctcctgct actaacagac ttgctactca ctgggaaccc 650  
 tgccgtgagg ctcaaactga gcgcctttgc tgcgtgttcc tctgtcctgt 700  
 caggtctcct ggggatggtg gccacatga tgtattcaca agtcttccaa 750  
 gcgactgtca acttgggtcc agaagactgg agaccacatg tttggaatta 800  
 tggctggggc ttctacatgg cctggctctc cttcacctgc tgcattgggt 850  
 cggctgtcac caccttcaac acgtacacca ggatggtgct ggagttcaag 900  
 tgcaagcata gtaagagctt caaggaaaac ccgaactgcc taccacatca 950  
 ccatcagtgt ttccctcggc ggctgtcaag tgcagcccc accgtgggtc 1000  
 ctttgaccag ctaccaccag tatcataatc agcccatcca ctctgtctct 1050  
 gagggagtgc acttctactc cgagctgcgg aacaaggat ttcaaagagg 1100  
 ggccagccag gagctgaaag aagcagttag gtcattctgta gaggaagagc 1150  
 agtgtttaga gttaagcggg tttggggagt aggccttgagc cctaccttac 1200  
 acgtctgctg attatcaaca tgtgtttaag ccaacatccg tctcttgagc 1250  
 atggttttta gaggctacga ataaggctat gaataagggt tatctttaag 1300  
 tcctaaggga ttccctgggtg ccaactgctct cttttcctct acagctccat 1350  
 cttgtttcac ccacccacaca tctcacacat ccagaattcc cttctttact 1400  
 gatagtttct gtgccagggt ctgggctaaa ccatggagat aaaaagaaga 1450  
 gtaaaatata cttcccgacc ttaaggatct gaaa 1484

<210> 272

<211> 285

<212> PRT

<213> Homo sapiens

<400> 272

Met	Ala	Lys	Met	Glu	Leu	Ser	Lys	Ala	Phe	Ser	Gly	Gln	Arg	Thr
1				5					10					15

Leu	Leu	Ser	Ala	Ile	Leu	Ser	Met	Leu	Ser	Leu	Ser	Phe	Ser	Thr
				20					25					30

Thr	Ser	Leu	Leu	Ser	Asn	Tyr	Trp	Phe	Val	Gly	Thr	Gln	Lys	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45				
Pro	Lys	Pro	Leu	Cys	Glu	Lys	Gly	Leu	Ala	Ala	Lys	Cys	Phe	Asp
				50					55					60
Met	Pro	Val	Ser	Leu	Asp	Gly	Asp	Thr	Asn	Thr	Ser	Thr	Gln	Glu
				65					70					75
Val	Val	Gln	Tyr	Asn	Trp	Glu	Thr	Gly	Asp	Asp	Arg	Phe	Ser	Phe
				80					85					90
Arg	Ser	Phe	Arg	Ser	Gly	Met	Trp	Leu	Ser	Cys	Glu	Glu	Thr	Val
				95					100					105
Glu	Glu	Pro	Gly	Glu	Arg	Cys	Arg	Ser	Phe	Ile	Glu	Leu	Thr	Pro
				110					115					120
Pro	Ala	Lys	Arg	Gly	Glu	Lys	Gly	Leu	Leu	Glu	Phe	Ala	Thr	Leu
				125					130					135
Gln	Gly	Pro	Cys	His	Pro	Thr	Leu	Arg	Phe	Gly	Gly	Lys	Arg	Leu
				140					145					150
Met	Glu	Lys	Ala	Ser	Leu	Pro	Ser	Pro	Pro	Leu	Gly	Leu	Cys	Gly
				155					160					165
Lys	Asn	Pro	Met	Val	Ile	Pro	Gly	Asn	Ala	Asp	His	Leu	His	Arg
				170					175					180
Thr	Ser	Ile	His	Gln	Leu	Pro	Pro	Ala	Thr	Asn	Arg	Leu	Ala	Thr
				185					190					195
His	Trp	Glu	Pro	Cys	Leu	Trp	Ala	Gln	Thr	Glu	Arg	Leu	Cys	Cys
				200					205					210
Cys	Phe	Leu	Cys	Pro	Val	Arg	Ser	Pro	Gly	Asp	Gly	Gly	Pro	His
				215					220					225
Asp	Val	Phe	Thr	Ser	Leu	Pro	Ser	Asp	Cys	Gln	Leu	Gly	Ser	Arg
				230					235					240
Arg	Leu	Glu	Thr	Thr	Cys	Leu	Glu	Leu	Trp	Leu	Gly	Leu	Leu	His
				245					250					255
Gly	Leu	Ala	Leu	Leu	His	Leu	Leu	His	Gly	Val	Gly	Cys	His	His
				260					265					270
Leu	Gln	His	Val	His	Gln	Asp	Gly	Ala	Gly	Val	Gln	Val	Gln	Ala
				275					280					285

<210> 273  
 <211> 1158  
 <212> DNA  
 <213> Homo sapiens

<400> 273  
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 ctcaacttaag tctcaggcct gtcagcagct cctgtggaca ttgccatccc 150  
 ctctggttagc cttcagagca aacaggacaa cctatgttat ggatgtttcc 200

accaaccagg gtagtggcat ggagcacctg aaccatctgt gcttctgtga 250  
 tctctatgac agagccactt ctccacctot gaaatgttcc ctgctctgaa 300  
 atctggcatg agatggcaca ggtgaccacg cagaagccac cagaatcttg 350  
 cctgccctat tcttcctccc aagtctgttc tottattgtc aacctcagca 400  
 caacaggctg gcgccaatgg cattacagag aaagcaatct gtgtggctag 450  
 tgggcagatt accatgcaag ccccgaggaga aatggaggag cttttagacc 500  
 acctccctgt cagccagtat taacatgtcc ccttccccct gccccgccgt 550  
 agattcagga cattcgcccc tgtgtgccac caaaccagga ctttccccct 600  
 ggcttggcat ccttggtctt ctctgggtac ccagcaagac gtctgttcca 650  
 gggcagtgtg gcatctttca agctccgtta ctatggcgat ggccatgatg 700  
 ttacaatccc acttgccctga ataataaagt gggaagggga agcagaggga 750  
 aatggggcca tgtgaatgca gctgctctgt tctccctacc ctgaggaaaa 800  
 accaaaggga agcaacagga acttctgcaa ctggttttta tcggaaagat 850  
 catcctgcct gcagatgctg ttgaaggggc acaagaaatg tagctggaga 900  
 agattgatga aagtgcaggt gtgtaaggaa atagaacagt ctgctgggag 950  
 tcagacctgg aattctgatt ccaaactctt tattactttg ggaagtcact 1000  
 cagcctcccc gtagccatct ccagggtgac ggaaccaggt gtattacctg 1050  
 ctggaaccaa ggaaactaac aatgtaggtt actagtgaat accccaatgg 1100  
 tttctccaat tatgcccatg ccaccaaacc aataaaacaa aattctctaa 1150  
 cactgaaa 1158

<210> 274  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 274  
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 Leu Leu Trp Thr Leu Pro Ser Pro Leu Val Ala Phe Arg Ala Asn  
 35 40 45  
 Arg Thr Thr Tyr Val Met Asp Val Ser Thr Asn Gln Gly Ser Gly  
 50 55 60  
 Met Glu His Arg Asn His Leu Cys Phe Cys Asp Leu Tyr Asp Arg  
 65 70 75  
 Ala Thr Ser Pro Pro Leu Lys Cys Ser Leu Leu  
 80 85

<210> 275  
<211> 2694  
<212> DNA  
<213> Homo sapiens

<400> 275  
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tttacatcct ttcacctatt ccatactgca tagcaagaag attagtggat 250  
gatacagatg ctatgagtaa cgottgtaag gaacttgcca tctttcttac 300  
aacgggcatt gtcgtgtcag cttttggact ccctattgta tttgccagag 350  
cacatctgat tgagtgggga gcttgtgcac ttgttctcac aggaaacaca 400  
gtcatctttg caactatact aggccttttc ttggctcttg gaagcaatga 450  
cgacttcagc tggcagcagt ggtgaaaaga aattactgaa ctattgtcaa 500  
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actcagtgc aatatagctg catttatacc tcagaggggc caagtgttaa 1050  
tgcccatgcc ctccgttaag ggttgttggt tttactggta gacagatgtt 1100  
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tctcaattgt tagaagaatt tatgttaaac ttaaggtaa ggggtgaaaa 1200  
acatttttga gataagggtt ttatttatgt ttattattgt tagagtgagt 1250  
tgcaatgtgg gaagaaatga cattgaaatt ccagtttttg aatcctgttt 1300  
ctattttataa gtgaaatttg tgatctccta tcaacctttc atgttttacc 1350  
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<210> 276  
<211> 131  
<212> PRT  
<213> Homo sapiens

<400> 276  
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Ile Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr  
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Asn Lys Tyr Trp Pro Leu Phe Val Leu Phe Phe Tyr Ile Leu Ser

Pro	Ile	Pro	Tyr	Cys	Ile	Ala	Arg	Arg	Leu	Val	Asp	Asp	Thr	Asp	35	40	45
				50					55					60			
Ala	Met	Ser	Asn	Ala	Cys	Lys	Glu	Leu	Ala	Ile	Phe	Leu	Thr	Thr	65	70	75
Gly	Ile	Val	Val	Ser	Ala	Phe	Gly	Leu	Pro	Ile	Val	Phe	Ala	Arg	80	85	90
Ala	His	Leu	Ile	Glu	Trp	Gly	Ala	Cys	Ala	Leu	Val	Leu	Thr	Gly	95	100	105
Asn	Thr	Val	Ile	Phe	Ala	Thr	Ile	Leu	Gly	Phe	Phe	Leu	Val	Phe	110	115	120
Gly	Ser	Asn	Asp	Asp	Phe	Ser	Trp	Gln	Gln	Trp					125	130	

<210> 277  
 <211> 4104  
 <212> DNA  
 <213> Homo sapiens

<400> 277  
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 cgccgcgcgc cgcacctccc caccgcccgc cgccgcgcgc ccgcccgcgc 200  
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<210> 278  
 <211> 522  
 <212> PRT  
 <213> Homo sapiens

<400> 278

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Arg	Pro	Ser	Gly	Val	Val	Leu	Cys	Leu	Leu	Gly	Ala	Cys	Phe	Gln	20	25	30	
Met	Leu	Pro	Ala	Ala	Pro	Ser	Gly	Cys	Pro	Gln	Leu	Cys	Arg	Cys	35	40	45	
Glu	Gly	Arg	Leu	Leu	Tyr	Cys	Glu	Ala	Leu	Asn	Leu	Thr	Glu	Ala	50	55	60	
Pro	His	Asn	Leu	Ser	Gly	Leu	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	65	70	75	
Ser	Leu	Ser	Glu	Leu	Arg	Ala	Gly	Gln	Phe	Thr	Gly	Leu	Met	Gln	80	85	90	
Leu	Thr	Trp	Leu	Tyr	Leu	Asp	His	Asn	His	Ile	Cys	Ser	Val	Gln	95	100	105	
Gly	Asp	Ala	Phe	Gln	Lys	Leu	Arg	Arg	Val	Lys	Glu	Leu	Thr	Leu	110	115	120	
Ser	Ser	Asn	Gln	Ile	Thr	Gln	Leu	Pro	Asn	Thr	Thr	Phe	Arg	Pro	125	130	135	
Met	Pro	Asn	Leu	Arg	Ser	Val	Asp	Leu	Ser	Tyr	Asn	Lys	Leu	Gln	140	145	150	
Ala	Leu	Ala	Pro	Asp	Leu	Phe	His	Gly	Leu	Arg	Lys	Leu	Thr	Thr	155	160	165	
Leu	His	Met	Arg	Ala	Asn	Ala	Ile	Gln	Phe	Val	Pro	Val	Arg	Ile	170	175	180	
Phe	Gln	Asp	Cys	Arg	Ser	Leu	Lys	Phe	Leu	Asp	Ile	Gly	Tyr	Asn	185	190	195	
Gln	Leu	Lys	Ser	Leu	Ala	Arg	Asn	Ser	Phe	Ala	Gly	Leu	Phe	Lys	200	205	210	
Leu	Thr	Glu	Leu	His	Leu	Glu	His	Asn	Asp	Leu	Val	Lys	Val	Asn	215	220	225	
Phe	Ala	His	Phe	Pro	Arg	Leu	Ile	Ser	Leu	His	Ser	Leu	Cys	Leu	230	235	240	
Arg	Arg	Asn	Lys	Val	Ala	Ile	Val	Val	Ser	Ser	Leu	Asp	Trp	Val	245	250	255	
Trp	Asn	Leu	Glu	Lys	Met	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Tyr	260	265	270	
Met	Glu	Pro	His	Val	Phe	Glu	Thr	Val	Pro	His	Leu	Gln	Ser	Leu	275	280	285	

Gln	Leu	Asp	Ser	Asn	Arg	Leu	Thr	Tyr	Ile	Glu	Pro	Arg	Ile	Leu	290	295	300
Asn	Ser	Trp	Lys	Ser	Leu	Thr	Ser	Ile	Thr	Leu	Ala	Gly	Asn	Leu	305	310	315
Trp	Asp	Cys	Gly	Arg	Asn	Val	Cys	Ala	Leu	Ala	Ser	Trp	Leu	Ser	320	325	330
Asn	Phe	Gln	Gly	Arg	Tyr	Asp	Gly	Asn	Leu	Gln	Cys	Ala	Ser	Pro	335	340	345
Glu	Tyr	Ala	Gln	Gly	Glu	Asp	Val	Leu	Asp	Ala	Val	Tyr	Ala	Phe	350	355	360
His	Leu	Cys	Glu	Asp	Gly	Ala	Glu	Pro	Thr	Ser	Gly	His	Leu	Leu	365	370	375
Ser	Ala	Val	Thr	Asn	Arg	Ser	Asp	Leu	Gly	Pro	Pro	Ala	Ser	Ser	380	385	390
Ala	Thr	Thr	Leu	Ala	Asp	Gly	Gly	Glu	Gly	Gln	His	Asp	Gly	Thr	395	400	405
Phe	Glu	Pro	Ala	Thr	Val	Ala	Leu	Pro	Gly	Gly	Glu	His	Ala	Glu	410	415	420
Asn	Ala	Val	Gln	Ile	His	Lys	Val	Val	Thr	Gly	Thr	Met	Ala	Leu	425	430	435
Ile	Phe	Ser	Phe	Leu	Ile	Val	Val	Leu	Val	Leu	Tyr	Val	Ser	Trp	440	445	450
Lys	Cys	Phe	Pro	Ala	Ser	Leu	Arg	Gln	Leu	Arg	Gln	Cys	Phe	Val	455	460	465
Thr	Gln	Arg	Arg	Lys	Gln	Lys	Gln	Lys	Gln	Thr	Met	His	Gln	Met	470	475	480
Ala	Ala	Met	Ser	Ala	Gln	Glu	Tyr	Tyr	Val	Asp	Tyr	Lys	Pro	Asn	485	490	495
His	Ile	Glu	Gly	Ala	Leu	Val	Ile	Ile	Asn	Glu	Tyr	Gly	Ser	Cys	500	505	510
Thr	Cys	His	Gln	Gln	Pro	Ala	Arg	Glu	Cys	Glu	Val				515	520	

<210> 279

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 279

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<210> 280

<211> 709

<212> DNA

<213> Homo sapiens

<400> 280

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cacggacttc gacgtcgcag ccaactggag ccagaaccgg accccgtgcg 150  
ccggcggcgc cgttgagttc ccggcggaca agatgggtgc agtcctgggtg 200  
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<210> 281

<211> 229

<212> PRT

<213> Homo sapiens

<400> 281

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Leu	Thr	Gln	Ala	Val	Ser	Lys	Leu	Trp	Val	Pro	Asn	Thr	Asp	Phe
			20						25					30
Asp	Val	Ala	Ala	Asn	Trp	Ser	Gln	Asn	Arg	Thr	Pro	Cys	Ala	Gly
			35						40					45
Gly	Ala	Val	Glu	Phe	Pro	Ala	Asp	Lys	Met	Val	Ser	Val	Leu	Val
			50						55					60
Gln	Glu	Gly	His	Ala	Val	Ser	Asp	Met	Leu	Leu	Pro	Leu	Asp	Gly
			65						70					75
Glu	Leu	Val	Leu	Ala	Ser	Gly	Ala	Gly	Phe	Gly	Val	Ser	Asp	Val
			80						85					90
Gly	Ser	His	Leu	Asp	Cys	Gly	Ala	Gly	Glu	Pro	Ala	Val	Phe	Arg
			95						100					105
Asp	Ser	Asp	Arg	Phe	Ser	Trp	His	Asp	Pro	His	Leu	Trp	Arg	Ser
			110						115					120
Gly	Asp	Glu	Ala	Pro	Gly	Leu	Phe	Phe	Val	Asp	Ala	Glu	Arg	Val
			125						130					135

Pro	Cys	Arg	His	Asp	Asp	Val	Phe	Phe	Pro	Pro	Ser	Ala	Ser	Phe
				140					145					150
Arg	Val	Gly	Leu	Gly	Pro	Gly	Ala	Ser	Pro	Val	Arg	Val	Arg	Ser
				155					160					165
Ile	Ser	Ala	Leu	Gly	Arg	Thr	Phe	Thr	Arg	Asp	Glu	Asp	Leu	Ala
				170					175					180
Val	Phe	Leu	Ala	Ser	Arg	Ala	Gly	Arg	Leu	Arg	Phe	His	Gly	Pro
				185					190					195
Gly	Ala	Leu	Ser	Val	Gly	Pro	Glu	Asp	Cys	Ala	Asp	Pro	Ser	Gly
				200					205					210
Cys	Val	Cys	Gly	Asn	Ala	Glu	Ala	Gln	Pro	Trp	Ile	Cys	Ala	Ala
				215					220					225

Leu Leu Gln Pro

<210> 282  
 <211> 644  
 <212> DNA  
 <213> Homo sapiens

<400> 282  
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 gaagcgaatg ttgagccta ctggtttgat tgcaactatc atggtgctgt 100  
 tgtgttttgc acttaccctg tgttctgcct tttggtggca taacaaggga 150  
 cttgcactta tcttctgcat tttgcagtct ttggcattga cgtggtacag 200  
 cctttccttc ataccatttg caagggatgc tgtgaagaag tgttttgccg 250  
 tgtgtcttgc ataattcatg gccagtttta tgaagctttg gaaggcacta 300  
 tggacagaag ctggtggaca gttttgtaac tatcttcgaa acctctgtct 350  
 tacagacatg tgccttttat cttgcagcaa tgtgttgctt gtgattcgaa 400  
 catttgaggg ttacttttgg aagcaacaat acattctcga acctgaatgt 450  
 cagtagcaca ggatgagaag tgggttctgt atcttgtgga gtggaatctt 500  
 cctcatgtac ctgtttcctc tctggatgtt gtccactga attcccatga 550  
 atacaaacct attcagcaac agcaaaaaaa aaaaaaaaaa aaaaaaaaaa 600  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 644

<210> 283  
 <211> 77  
 <212> PRT  
 <213> Homo sapiens

<400> 283  
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 Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr Leu

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Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe					
	35		40		45
Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe					
	50		55		60
Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys					
	65		70		75
Leu Ala					

<210> 284  
 <211> 2623  
 <212> DNA  
 <213> Homo sapiens

<400> 284  
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 ctcccggttg tccaaactaa tacggactga acggatcgct gcgaggggtg 150  
 gagagaaaat tagggggaga aaggacagag agagcaacta ccatccatag 200  
 ccagatagat tatcttacac tgaactgac aagtactttg aaaatgactt 250  
 cgaaatttat cttggtgtcc ttcatacttg ctgcactgag tctttcaacc 300  
 accttttctc tccaactaga ccagcaaaag gttctactag tttcttttga 350  
 tggattccgt tgggattact tatataaagt tccaacgccc cattttcatt 400  
 atattatgaa atatggtgtt cacgtgaagc aagttactaa tgtttttatt 450  
 acaaaaacct accctaacca ttatactttg gtaactggcc tctttgcaga 500  
 gaatcatggg attgttgcaa atgatatgtt tgatcctatt cggaacaaat 550  
 ctttctcctt ggatcacatg aatatttatg attccaagtt ttgggaagaa 600  
 gcgacaccaa tatggatcac aaaccagagg gcaggacata ctagtgggtg 650  
 agccatgttg cccggaacag atgtaaaaat acataagcgc tttcctactc 700  
 attacatgcc ttacaatgag tcagtttcat ttgaagatag agttgccaaa 750  
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 ttgggaagac cctgatgaca tgggccacca tttgggacct gacagtccgc 850  
 tcatggggcc tgtcatttca gatattgaca agaagttagg atatctcata 900  
 caaatgctga aaaaggcaaa gttgtggaac actctgaacc taatcatcac 950  
 aagtgatcat ggaatgacgc agtgctctga ggaaaggta atagaacttg 1000  
 accagtacct ggataaagac cactataccc tgattgatca atctccagta 1050  
 gcagccatct tgccaaaaga aggtaaattt gatgaagtct atgaagcact 1100

aactcacgct catcctaatac ttactgttta caaaaaagaa gacgttccag 1150  
aaaggtggca ttacaaatac aacagtcgaa ttcaaccaat catagcagtg 1200  
gctgatgaag ggtggcacat ttacagaat aagtcagatg actttctgtt 1250  
aggcaaccac ggttacgata atgogtttagc agatatgcat ccaatatttt 1300  
tagcccatgg tcctgccttc agaaagaatt tctcaaaaga agccatgaac 1350  
tccacagatt tgtaccact actatgccac ctctcaata tcaactgcat 1400  
gccacacaat ggatcattct ggaatgtcca ggatctgctc aattcagcaa 1450  
tgccaagggt ggtcccttat acacagagta ctatactcct ccctggtagt 1500  
gttaaaccag cagaatatga ccaagagggg tcataccctt atttcatagg 1550  
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atggacagtt atgtcttata acttgattga aaatgacaac tttttgcacc 2100  
catgtcacag aatacttggt acgcattgtt caaactgaag gaaatttcta 2150  
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aagaagggtga taagtgttga aaattaaatg tgataacott tgaacottga 2250  
atatttgaga tgtattccca acagcagaat gcaactgtgg gcatttcttg 2300  
tcttatttct ttccagagaa cgtgggtttc atttattttt ccttcaaaag 2350  
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aagacaccat gaatatactt ttcttctata tagttcagca atggcctgaa 2500  
tagaagcaac caggcaccat ctgagcaatg ttttctcttg tttgtaatta 2550  
tttgctcctt tgaaaattaa atcactatta attacattaa aaatcaaatt 2600  
ggataaaaaa aaaaaaaaaa aaa 2623

<210> 285

<211> 477  
 <212> PRT  
 <213> Homo sapiens

<400> 285

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Ser	Leu	Ser	Thr	Thr	Phe	Ser	Leu	Gln	Leu	Asp	Gln	Gln	Lys	Val	
				20					25					30	
Leu	Leu	Val	Ser	Phe	Asp	Gly	Phe	Arg	Trp	Asp	Tyr	Leu	Tyr	Lys	
				35					40					45	
Val	Pro	Thr	Pro	His	Phe	His	Tyr	Ile	Met	Lys	Tyr	Gly	Val	His	
				50					55					60	
Val	Lys	Gln	Val	Thr	Asn	Val	Phe	Ile	Thr	Lys	Thr	Tyr	Pro	Asn	
				65					70					75	
His	Tyr	Thr	Leu	Val	Thr	Gly	Leu	Phe	Ala	Glu	Asn	His	Gly	Ile	
				80					85					90	
Val	Ala	Asn	Asp	Met	Phe	Asp	Pro	Ile	Arg	Asn	Lys	Ser	Phe	Ser	
				95					100					105	
Leu	Asp	His	Met	Asn	Ile	Tyr	Asp	Ser	Lys	Phe	Trp	Glu	Glu	Ala	
				110					115					120	
Thr	Pro	Ile	Trp	Ile	Thr	Asn	Gln	Arg	Ala	Gly	His	Thr	Ser	Gly	
				125					130					135	
Ala	Ala	Met	Trp	Pro	Gly	Thr	Asp	Val	Lys	Ile	His	Lys	Arg	Phe	
				140					145					150	
Pro	Thr	His	Tyr	Met	Pro	Tyr	Asn	Glu	Ser	Val	Ser	Phe	Glu	Asp	
				155					160					165	
Arg	Val	Ala	Lys	Ile	Val	Glu	Trp	Phe	Thr	Ser	Lys	Glu	Pro	Ile	
				170					175					180	
Asn	Leu	Gly	Leu	Leu	Tyr	Trp	Glu	Asp	Pro	Asp	Asp	Met	Gly	His	
				185					190					195	
His	Leu	Gly	Pro	Asp	Ser	Pro	Leu	Met	Gly	Pro	Val	Ile	Ser	Asp	
				200					205					210	
Ile	Asp	Lys	Lys	Leu	Gly	Tyr	Leu	Ile	Gln	Met	Leu	Lys	Lys	Ala	
				215					220					225	
Lys	Leu	Trp	Asn	Thr	Leu	Asn	Leu	Ile	Ile	Thr	Ser	Asp	His	Gly	
				230					235					240	
Met	Thr	Gln	Cys	Ser	Glu	Glu	Arg	Leu	Ile	Glu	Leu	Asp	Gln	Tyr	
				245					250					255	
Leu	Asp	Lys	Asp	His	Tyr	Thr	Leu	Ile	Asp	Gln	Ser	Pro	Val	Ala	
				260					265					270	
Ala	Ile	Leu	Pro	Lys	Glu	Gly	Lys	Phe	Asp	Glu	Val	Tyr	Glu	Ala	
				275					280					285	
Leu	Thr	His	Ala	His	Pro	Asn	Leu	Thr	Val	Tyr	Lys	Lys	Glu	Asp	

290										295					300				
Val	Pro	Glu	Arg	Trp	His	Tyr	Lys	Tyr	Asn	Ser	Arg	Ile	Gln	Pro					
				305					310					315					
Ile	Ile	Ala	Val	Ala	Asp	Glu	Gly	Trp	His	Ile	Leu	Gln	Asn	Lys					
				320					325					330					
Ser	Asp	Asp	Phe	Leu	Leu	Gly	Asn	His	Gly	Tyr	Asp	Asn	Ala	Leu					
				335					340					345					
Ala	Asp	Met	His	Pro	Ile	Phe	Leu	Ala	His	Gly	Pro	Ala	Phe	Arg					
				350					355					360					
Lys	Asn	Phe	Ser	Lys	Glu	Ala	Met	Asn	Ser	Thr	Asp	Leu	Tyr	Pro					
				365					370					375					
Leu	Leu	Cys	His	Leu	Leu	Asn	Ile	Thr	Ala	Met	Pro	His	Asn	Gly					
				380					385					390					
Ser	Phe	Trp	Asn	Val	Gln	Asp	Leu	Leu	Asn	Ser	Ala	Met	Pro	Arg					
				395					400					405					
Val	Val	Pro	Tyr	Thr	Gln	Ser	Thr	Ile	Leu	Leu	Pro	Gly	Ser	Val					
				410					415					420					
Lys	Pro	Ala	Glu	Tyr	Asp	Gln	Glu	Gly	Ser	Tyr	Pro	Tyr	Phe	Ile					
				425					430					435					
Gly	Val	Ser	Leu	Gly	Ser	Ile	Ile	Val	Ile	Val	Phe	Phe	Val	Ile					
				440					445					450					
Phe	Ile	Lys	His	Leu	Ile	His	Ser	Gln	Ile	Pro	Ala	Leu	Gln	Asp					
				455					460					465					
Met	His	Ala	Glu	Ile	Ala	Gln	Pro	Leu	Leu	Gln	Ala								
				470					475										

<210> 286  
 <211> 1337  
 <212> DNA  
 <213> Homo sapiens

<400> 286  
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 agggaggtga agaaaccaag acgcagagag gccaagcccc ttgccttggg 150  
 tcacacagcc aaaggaggca gagccagaac tcacaaccag atccagaggc 200  
 aacagggaca tggccacctg ggacgaaaag gcagtcaccc gcagggccaa 250  
 ggtggctccc gctgagagga tgagcaagtt cttaaggcac ttcacggtcg 300  
 tgggagacga ctaccatgcc tggaacatca actacaagaa atgggagaa 350  
 gaagaggagg aggaggagga ggagcagcca ccaccacac cagtctcagg 400  
 cgaggaaggc agagctgcag cccctgacgt tgcccctgcc cctggccccg 450  
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tcccacaggt ttcaggtcat catcatctgc ttggtggttc tggatgccct 550  
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 agaataacta tgctgccatg gtattccact acatgagcat caccatcttg 650  
 gtctttttta tgatggagat catctttaaa ttatttgtct tccgcctgag 700  
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 cattcatcct ggacattgtc ctctgttcc aggagcacca gtttgaggct 800  
 ctgggcctgc tgattctgct cgggctgtgg cgggtggccc ggatcatcaa 850  
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 ctctcacaca gccaccgtga aagtcttgga gtaaaatgtg ctgtgtacag 1100  
 aagagagaga aggaagcagg ctggcatgtt cactgggctg gtgttaacgac 1150  
 agagaacctg acagtcactg gccagttatc acttcagatt acaaatacaca 1200  
 cagagcatct gcctgttttc aatcacaaga gaacaaaacc aaaatctata 1250  
 aagatattct gaaaatatga cagaatttga caaataaaaag cataaacgtg 1300  
 taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1337

<210> 287

<211> 255

<212> PRT

<213> Homo sapiens

<400> 287

Met	Ala	Thr	Trp	Asp	Glu	Lys	Ala	Val	Thr	Arg	Arg	Ala	Lys	Val
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Ala	Pro	Ala	Glu	Arg	Met	Ser	Lys	Phe	Leu	Arg	His	Phe	Thr	Val
			20						25				30	
Val	Gly	Asp	Asp	Tyr	His	Ala	Trp	Asn	Ile	Asn	Tyr	Lys	Lys	Trp
			35						40				45	
Glu	Asn	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gln	Pro	Pro	Pro	Thr
			50						55				60	
Pro	Val	Ser	Gly	Glu	Glu	Gly	Arg	Ala	Ala	Ala	Pro	Asp	Val	Ala
			65						70				75	
Pro	Ala	Pro	Gly	Pro	Ala	Pro	Arg	Ala	Pro	Leu	Asp	Phe	Arg	Gly
			80						85				90	
Met	Leu	Arg	Lys	Leu	Phe	Ser	Ser	His	Arg	Phe	Gln	Val	Ile	Ile
			95						100				105	
Ile	Cys	Leu	Val	Val	Leu	Asp	Ala	Leu	Leu	Val	Leu	Ala	Glu	Leu
			110						115				120	

Ile	Leu	Asp	Leu	Lys	Ile	Ile	Gln	Pro	Asp	Lys	Asn	Asn	Tyr	Ala	
				125					130					135	
Ala	Met	Val	Phe	His	Tyr	Met	Ser	Ile	Thr	Ile	Leu	Val	Phe	Phe	
				140					145					150	
Met	Met	Glu	Ile	Ile	Phe	Lys	Leu	Phe	Val	Phe	Arg	Leu	Ser	Ser	
				155					160					165	
Phe	Thr	Thr	Ser	Leu	Arg	Ser	Trp	Met	Pro	Val	Val	Val	Val	Val	
				170					175					180	
Ser	Phe	Ile	Leu	Asp	Ile	Val	Leu	Leu	Phe	Gln	Glu	His	Gln	Phe	
				185					190					195	
Glu	Ala	Leu	Gly	Leu	Leu	Ile	Leu	Leu	Arg	Leu	Trp	Arg	Val	Ala	
				200					205					210	
Arg	Ile	Ile	Asn	Gly	Ile	Ile	Ile	Ser	Val	Lys	Thr	Arg	Ser	Glu	
				215					220					225	
Arg	Gln	Leu	Leu	Arg	Leu	Lys	Gln	Met	Asn	Val	Gln	Leu	Ala	Ala	
				230					235					240	
Lys	Ile	Gln	His	Leu	Glu	Phe	Ser	Cys	Ser	Glu	Lys	Pro	Leu	Asp	
				245					250					255	

<210> 288  
 <211> 3334  
 <212> DNA  
 <213> Homo sapiens

<400> 288  
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 cccagaccga gttccagtac tttgagtcga aggggctccc tgccgagctg 150  
 aagtccattt tcaagctcag tgtcttcata cctcccagg aattotccac 200  
 ctaccgccag tggaagcaga aaattgtaca agctggagat aaggaccttg 250  
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 aagaagctga ggctggtgtt taagattttg gacaaaaaga atgatggacg 350  
 cattgacgcg caggagatca tgcagtccct gcgggacttg ggagtcaaga 400  
 tatctgaaca gcaggcagaa aaaattctca agagcatgga taaaaacggc 450  
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 cgtggaaaac atccccgaga tcatcctota ctggaagcat tccacgatct 550  
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 aggcagacgg ggatgtggtg gagacacctg gtggcaggag gtggggcagg 650  
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actcagatga ttcgagaagg agggggccagg tcaactctggc ggggcaatgg 800  
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 catctacca atggagggtc tgaagaccg gatggcgctg cggaagacag 1000  
 gccagtactc aggaatgctg gactgcgcca ggaggatcct ggccagagag 1050  
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 ggctgcagca ctatgcagtg aacagcgcgg accccggcgt gtttgtgctc 1200  
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 cccagctgtg agcatcagct acgtggtcta cgagaacctg aagatcacc 1450  
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 cgcagggagg gtggggagag ctggcaggcc cagggttgt cctgctgacc 1650  
 ccagcagacc ctctgtttg ttccagcgaa gaccacaggc attccttagg 1700  
 gtccagggtc agcaggctcc gggctcacat gtgtaaggac aggacatttt 1750  
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 tctgccgtgc atctccctgt gccctcttgc tgccctgctg tctgctgagg 1900  
 taaggtggga ggagggtac agcccacatc ccacccctc gtccaatccc 1950  
 ataatccatg atgaaagggt aggtcacgtg gcctcccagg cctgacttcc 2000  
 caacctacag cattgacgcc aacttggtg tgaaggaaga ggaaaggatc 2050  
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 ggcatgcttg ggagtgcagg gggctcgggc tgccctggcct ggctgcacag 2150  
 aaggcaagtg ctggggctca tgggtgctctg agctggcctg gaccctgtca 2200  
 ggatggggcc cacctcagaa ccaaaactcac tgtccccact gtggcatgag 2250  
 ggcagtggag caccatgttt gagggcgaag ggcagagcgt ttgtgtgttc 2300  
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aaagggtttt gtccagaagg acaagccgga caaatgagcg acttctgtgc 2400  
 ttccagagga agacgagggg gcaggagctt ggctgactgc tcagagtctg 2450  
 ttctgacgcc ctgggggttc ctgtccaacc ccagcagggg cgcagcggga 2500  
 ccagccccac attccacttg tgtcactgct tggaacctat ttatattgta 2550  
 tttatttgaa cagagttatg tcctaactat ttttatagat ttgtttaatt 2600  
 aatagcttgt cattttcaag ttcatTTTTT attcatattt atgttcatgg 2650  
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 ggggggcctt gggccgtgc agtcacatct gtccagagaa attccttttg 2750  
 ggactggagg cagaaaagcg gccagaaggc agcagccctg gctcctttcc 2800  
 tttggcaggt tggggaaggg cttgccccca gccttaggat ttcagggttt 2850  
 gactgggggc gtggagagag agggaggaac ctcaataacc ttgaaggtgg 2900  
 aatccagtta tttcctgcgc tgcgagggtt tctttatttc actcttttct 2950  
 gaatgtcaag gcagtgaggt gcctctcact gtgaatttgt ggtgggcggg 3000  
 ggctggagga gaggtgggg ggctggctcc gtccctccca gccttctgct 3050  
 gcccttgctt aacaatgccg gccaaactggc gacctcacgg ttgcacttcc 3100  
 attccaccag aatgacctga tgaggaaatc ttcaatagga tgcaaagatc 3150  
 aatgcaaaaa ttgttatata tgaacatata actggagtcg tcaaaaagca 3200  
 aattaagaaa gaattggacg ttagaagttg tcatttaaag cagccttcta 3250  
 ataaagttgt ttcaaagctg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3300  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 3334

<210> 289  
 <211> 469  
 <212> PRT  
 <213> Homo sapiens

<400> 289  
 Met Leu Cys Leu Cys Leu Tyr Val Pro Val Ile Gly Glu Ala Gln  
 1 5 10 15  
 Thr Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu  
 20 25 30  
 Lys Ser Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe  
 35 40 45  
 Ser Thr Tyr Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp  
 50 55 60  
 Lys Asp Leu Asp Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr  
 65 70 75  
 Leu Gln Asp His Glu Lys Lys Leu Arg Leu Val Phe Lys Ile Leu  
 80 85 90

Asp	Lys	Lys	Asn	Asp	Gly	Arg	Ile	Asp	Ala	Gln	Glu	Ile	Met	Gln	95	100	105
Ser	Leu	Arg	Asp	Leu	Gly	Val	Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu	110	115	120
Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys	Asn	Gly	Thr	Met	Thr	Ile	Asp	125	130	135
Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu	Leu	His	Pro	Val	Glu	Asn	140	145	150
Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His	Ser	Thr	Ile	Phe	Asp	155	160	165
Val	Gly	Glu	Asn	Leu	Thr	Val	Pro	Asp	Glu	Phe	Thr	Val	Glu	Glu	170	175	180
Arg	Gln	Thr	Gly	Met	Trp	Trp	Arg	His	Leu	Val	Ala	Gly	Gly	Gly	185	190	195
Ala	Gly	Ala	Val	Ser	Arg	Thr	Cys	Thr	Ala	Pro	Leu	Asp	Arg	Leu	200	205	210
Lys	Val	Leu	Met	Gln	Val	His	Ala	Ser	Arg	Ser	Asn	Asn	Met	Gly	215	220	225
Ile	Val	Gly	Gly	Phe	Thr	Gln	Met	Ile	Arg	Glu	Gly	Gly	Ala	Arg	230	235	240
Ser	Leu	Trp	Arg	Gly	Asn	Gly	Ile	Asn	Val	Leu	Lys	Ile	Ala	Pro	245	250	255
Glu	Ser	Ala	Ile	Lys	Phe	Met	Ala	Tyr	Glu	Gln	Ile	Lys	Arg	Leu	260	265	270
Val	Gly	Ser	Asp	Gln	Glu	Thr	Leu	Arg	Ile	His	Glu	Arg	Leu	Val	275	280	285
Ala	Gly	Ser	Leu	Ala	Gly	Ala	Ile	Ala	Gln	Ser	Ser	Ile	Tyr	Pro	290	295	300
Met	Glu	Val	Leu	Lys	Thr	Arg	Met	Ala	Leu	Arg	Lys	Thr	Gly	Gln	305	310	315
Tyr	Ser	Gly	Met	Leu	Asp	Cys	Ala	Arg	Arg	Ile	Leu	Ala	Arg	Glu	320	325	330
Gly	Val	Ala	Ala	Phe	Tyr	Lys	Gly	Tyr	Val	Pro	Asn	Met	Leu	Gly	335	340	345
Ile	Ile	Pro	Tyr	Ala	Gly	Ile	Asp	Leu	Ala	Val	Tyr	Glu	Thr	Leu	350	355	360
Lys	Asn	Ala	Trp	Leu	Gln	His	Tyr	Ala	Val	Asn	Ser	Ala	Asp	Pro	365	370	375
Gly	Val	Phe	Val	Leu	Leu	Ala	Cys	Gly	Thr	Met	Ser	Ser	Thr	Cys	380	385	390
Gly	Gln	Leu	Ala	Ser	Tyr	Pro	Leu	Ala	Leu	Val	Arg	Thr	Arg	Met	395	400	405

Gln	Ala	Gln	Ala	Ser	Ile	Glu	Gly	Ala	Pro	Glu	Val	Thr	Met	Ser
				410					415					420
Ser	Leu	Phe	Lys	His	Ile	Leu	Arg	Thr	Glu	Gly	Ala	Phe	Gly	Leu
				425					430					435
Tyr	Arg	Gly	Leu	Ala	Pro	Asn	Phe	Met	Lys	Val	Ile	Pro	Ala	Val
				440					445					450
Ser	Ile	Ser	Tyr	Val	Val	Tyr	Glu	Asn	Leu	Lys	Ile	Thr	Leu	Gly
				455					460					465
Val Gln Ser Arg														

<210> 290  
 <211> 1658  
 <212> DNA  
 <213> Homo sapiens

<400> 290  
 ggaaggcagc ggcagctcca ctgagccagt acccagatac gctgggaacc 50  
 ttccccagcc atggcttccc tggggcagat cctcttctgg agcataatta 100  
 gcatcatcat tattctggct ggagcaattg cactcatcat tggctttggt 150  
 atttcaggga gacactccat cacagtcact actgtcgct cagctgggaa 200  
 cattggggag gatggaatcc tgagctgcac ttttgaacct gacatcaaac 250  
 tttctgatat cgtgatacaa tggctgaagg aagggtgttt aggcttggtc 300  
 catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatggt 350  
 cagaggccgg acagcagtgt ttgctgatca agtgatagtt ggcaatgcct 400  
 ctttgccggt gaaaaacgtg caactcacag atgctggcac ctacaaatgt 450  
 tatatcatca cttctaaagg caaggggaat gctaaccttg agtataaaac 500  
 tggagccttc agcatgccgg aagtgaatgt ggactataat gccagctcag 550  
 agaccttgcg gtgtgaggct ccccgatggt tccccagcc cacagtgggtc 600  
 tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 650  
 cagctttgag ctgaactctg agaatgtgac catgaagggt gtgtctgtgc 700  
 tctacaatgt tacgatcaac aacacatact cctgtatgat tgaaaatgac 750  
 attgccaaag caacagggga tatcaaagt acagaatcgg agatcaaaaag 800  
 gggagtcac ctacagctgc taaactcaaa ggcttctctg tgtgtctctt 850  
 ctttctttgc catcagctgg gcacttctgc ctctcagccc ttacctgatg 900  
 ctaaaataat gtgccttggc cacaataaag catgcaaagt cattgttaca 950  
 acagggatct acagaactat ttcaccacca gatatgacct agttttatat 1000  
 ttctgggagg aaatgaattc atatctagaa gtctggagt agcaaacaag 1050

agcaagaaac aaaaagaagc caaaagcaga aggcctcaat atgaacaaga 1100  
 taaatctatc ttcaaagaca tattagaagt tgggaaaata attcatgtga 1150  
 actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 1200  
 gcatccccag atctcaggga cctccccctg cctgtcacct ggggagtgag 1250  
 aggacaggat agtgcattgt ctttgtctct gaatttttag ttatatgtgc 1300  
 tgtaatgttg ctctgaggaa gcccctggaa agtctatccc aacatatcca 1350  
 catcttatat tccacaaatt aagctgtagt atgtacccta agacgctgct 1400  
 aattgactgc cacttcgcaa ctccggggcg gctgcatttt agtaatgggt 1450  
 caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 1500  
 ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa 1550  
 acagagcagt cggggacacc gattttataa ataaactgag caccttcttt 1600  
 tttaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
 aaaaaaaaa 1658

<210> 291  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<400> 291  
 Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile  
 1 5 10 15  
 Ile Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly  
 20 25 30  
 Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala  
 35 40 45  
 Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro  
 50 55 60  
 Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly  
 65 70 75  
 Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu  
 80 85 90  
 Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala  
 95 100 105  
 Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val  
 110 115 120  
 Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser  
 125 130 135  
 Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe  
 140 145 150  
 Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr

	155		160		165
Leu Arg Cys Glu	Ala Pro Arg Trp Phe	Pro Gln Pro Thr Val	Val		
	170	175	180		
Trp Ala Ser Gln	Val Asp Gln Gly Ala	Asn Phe Ser Glu Val	Ser		
	185	190	195		
Asn Thr Ser Phe	Glu Leu Asn Ser Glu	Asn Val Thr Met Lys	Val		
	200	205	210		
Val Ser Val Leu	Tyr Asn Val Thr Ile	Asn Asn Thr Tyr Ser	Cys		
	215	220	225		
Met Ile Glu Asn	Asp Ile Ala Lys Ala	Thr Gly Asp Ile Lys	Val		
	230	235	240		
Thr Glu Ser Glu	Ile Lys Arg Arg Ser	His Leu Gln Leu Leu	Asn		
	245	250	255		
Ser Lys Ala Ser	Leu Cys Val Ser Ser	Phe Phe Ala Ile Ser	Trp		
	260	265	270		
Ala Leu Leu Pro	Leu Ser Pro Tyr Leu	Met Leu Lys			
	275	280			

<210> 292  
 <211> 1484  
 <212> DNA  
 <213> Homo sapiens

<400> 292  
 gaatttgtag aagacagcgg cgttgccatg gcggcgctctc tggggcaggt 50  
 gttggctctg gtgctggtgg ccgctctgtg ggggtggcacg cagccgctgc 100  
 tgaagcgggc ctccgccggc ctgcagcggg ttcattgagcc gacctggggc 150  
 cagcagttgc tacaggagat gaagaccctc ttcttgaata ctgagtacct 200  
 gatgcccttt ctctcaacc agtgtggatc ccttctctat tacctcaact 250  
 tggcatcgac agatctgacc ctggctgtgc ccatctgtaa ctctctggct 300  
 atcatcttca cactgattgt tgggaaggcc cttggagaag atattggtgg 350  
 aaaacgtaag ttagactact gcgagtgcgg gacgcagctc tgtggatctc 400  
 gacataacctg tgtagttcc ttcccagaac ccatctcccc agagtgggtg 450  
 aggacacggc cttttcccat cctgcccttt cctctgcagc tgttttgctt 500  
 ccttggtggc atcagagttc cttcccctg gacagtctgg agaaagacag 550  
 aggctggggg ttgggattga agaccagacc ccatctgagc ccttctcca 600  
 gccctgtacc agctctact ggcatggctg agctcagacc ctctgattt 650  
 ctgcctatta tcccaggagc agttgctggc atggtgctca ccgtgatagg 700  
 aatttcactc tgcatacaaa gctcagtga taagaccagc gggcaacagt 750  
 ctaccctttg agtgggcca acccacttcc agctctgtg cctccaggaa 800

gcccctgggc catgaagtgc tggcagtgc cggatggacc tagcacttcc 850  
 cctctctggc cttagcttcc tcctctctta tggggataac agctacctca 900  
 tggatcacaa taagagaaca agagtgaag agttttgtaa ctttcaagtgc 950  
 ctgttcagct gcggggattt agcacaggag actctacgct caccctcagc 1000  
 aacctttctg cccagcagc tctcttcctg ctaacatctc aggctcccag 1050  
 cccagccacc attactgtgg cctgatctgg actatcatgg tggcaggttc 1100  
 catggactgc agaactccag ctgcatggaa agggccagct gcagactttg 1150  
 agccagaaat gcaaacggga ggcctctggg actcagtcag agcgctttgg 1200  
 ctgaatgagg ggtggaaccg agggaagaag gtgcgtcggg gtggcagatg 1250  
 caggaaatga gctgtctatt agccttgcct gccccaccca tgaggtaggc 1300  
 agaaatcctc actgccagcc cctcttaaac aggtagagag ctgtgagccc 1350  
 cagccccacc tgactccagc acacctggcg agtagtagct gtcaataaat 1400  
 ctatgtaaac agacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1484

<210> 293  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 293  
 Met Ala Ala Ser Leu Gly Gln Val Leu Ala Leu Val Leu Val Ala  
 1 5 10 15  
 Ala Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ala  
 20 25 30  
 Gly Leu Gln Arg Val His Glu Pro Thr Trp Ala Gln Gln Leu Leu  
 35 40 45  
 Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro  
 50 55 60  
 Phe Leu Leu Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr Leu  
 65 70 75  
 Ala Ser Thr Asp Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu  
 80 85 90  
 Ala Ile Ile Phe Thr Leu Ile Val Gly Lys Ala Leu Gly Glu Asp  
 95 100 105  
 Ile Gly Gly Lys Arg Lys Leu Asp Tyr Cys Glu Cys Gly Thr Gln  
 110 115 120  
 Leu Cys Gly Ser Arg His Thr Cys Val Ser Ser Phe Pro Glu Pro  
 125 130 135  
 Ile Ser Pro Glu Trp Val Arg Thr Arg Pro Phe Pro Ile Leu Pro  
 140 145 150

Phe	Pro	Leu	Gln	Leu	Phe	Cys	Phe	Leu	Val	Ala	Ile	Arg	Val	Pro
				155					160					165
Phe	Pro	Trp	Thr	Val	Trp	Arg	Lys	Thr	Glu	Ala	Gly	Val	Trp	Asp
				170					175					180

<210> 294  
 <211> 1164  
 <212> DNA  
 <213> Homo sapiens

<400> 294  
 cttctgtagg acagtcacca ggccagatcc agaagcctct ctaggctcca 50  
 gcttttctctg tggaagatga cagcaattat agcaggaccc tgccaggctg 100  
 tcgaaaagat tccgcaataa aactttgcca gtgggaagta cctagtgaaa 150  
 cggcctaaga tgccacttct tctcatgtcc caggcttgag gccctgtggt 200  
 ccccatcctt gggagaagtc agctccagca ccatgaaggg catcctcggt 250  
 gctggtatca ctgcagtgtc tgttgacagt gtagaatctc tgagctgcgt 300  
 gcagtgtaat tcatgggaaa aatcctgtgt caacagcatt gcctctgaat 350  
 gtccctcaca tgccaacacc agctgtatca gctcctcagc cagctcctct 400  
 ctagagacac cagtcagatt ataccagaat atgttctgct cagcggagaa 450  
 ctgcagtgtg gagacacaca ttacagcctt cactgtccac gtgtctgtg 500  
 aagaacactt tcattttgta agccagtgtc gccaaggaaa ggaatgcagc 550  
 aacaccagcg atgccctgga cctccccctg aagaacgtgt ccagcaacgc 600  
 agagtgcctt gcttggttatg aatctaattg aacttcctgt cgtgggaagc 650  
 cctggaaatg ctatgaagaa gaacagtgtg tctttctagt tgcagaactt 700  
 aagaatgaca ttgagtctaa gagtctctgt ctgaaaggct gttccaacgt 750  
 cagtaacgcc acctgtcagt tcctgtcttg tgaaaacaag actcttgag 800  
 gagtcatctt tcgaaagttt gagtgtgcaa atgtaaacag ctttaacccc 850  
 acgtctgcac caaccacttc ccacaacgtg ggctccaaag cttccctcta 900  
 cctcttggtc cttgccagcc tccttcttcg gggactgtc cctgaggtc 950  
 ctggggctgc actttgccca gcacccatt tctgcttctc tgagggtccag 1000  
 agcaccocct gcgggtgtga caccctcttt ccctgtcttg ccccgtttaa 1050  
 ctgccagta agtgggagtc acaggtctcc aggcaatgcc gacagctgcc 1100  
 ttgttttcca ttattaaagc actggttcat tcactgcaa aaaaaaaaaa 1150  
 aaaaaaaaaa aaaa 1164

<210> 295  
 <211> 237  
 <212> PRT

<213> Homo sapiens

<400> 295

Met	Lys	Gly	Ile	Leu	Val	Ala	Gly	Ile	Thr	Ala	Val	Leu	Val	Ala	
1				5					10					15	
Ala	Val	Glu	Ser	Leu	Ser	Cys	Val	Gln	Cys	Asn	Ser	Trp	Glu	Lys	
				20					25					30	
Ser	Cys	Val	Asn	Ser	Ile	Ala	Ser	Glu	Cys	Pro	Ser	His	Ala	Asn	
				35					40					45	
Thr	Ser	Cys	Ile	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Leu	Glu	Thr	Pro	
				50					55					60	
Val	Arg	Leu	Tyr	Gln	Asn	Met	Phe	Cys	Ser	Ala	Glu	Asn	Cys	Ser	
				65					70					75	
Glu	Glu	Thr	His	Ile	Thr	Ala	Phe	Thr	Val	His	Val	Ser	Ala	Glu	
				80					85					90	
Glu	His	Phe	His	Phe	Val	Ser	Gln	Cys	Cys	Gln	Gly	Lys	Glu	Cys	
				95					100					105	
Ser	Asn	Thr	Ser	Asp	Ala	Leu	Asp	Pro	Pro	Leu	Lys	Asn	Val	Ser	
				110					115					120	
Ser	Asn	Ala	Glu	Cys	Pro	Ala	Cys	Tyr	Glu	Ser	Asn	Gly	Thr	Ser	
				125					130					135	
Cys	Arg	Gly	Lys	Pro	Trp	Lys	Cys	Tyr	Glu	Glu	Glu	Gln	Cys	Val	
				140					145					150	
Phe	Leu	Val	Ala	Glu	Leu	Lys	Asn	Asp	Ile	Glu	Ser	Lys	Ser	Leu	
				155					160					165	
Val	Leu	Lys	Gly	Cys	Ser	Asn	Val	Ser	Asn	Ala	Thr	Cys	Gln	Phe	
				170					175					180	
Leu	Ser	Gly	Glu	Asn	Lys	Thr	Leu	Gly	Gly	Val	Ile	Phe	Arg	Lys	
				185					190					195	
Phe	Glu	Cys	Ala	Asn	Val	Asn	Ser	Leu	Thr	Pro	Thr	Ser	Ala	Pro	
				200					205					210	
Thr	Thr	Ser	His	Asn	Val	Gly	Ser	Lys	Ala	Ser	Leu	Tyr	Leu	Leu	
				215					220					225	
Ala	Leu	Ala	Ser	Leu	Leu	Leu	Arg	Gly	Leu	Leu	Pro				
				230					235						

<210> 296

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 296

ggcctcggtt caaacgaccc ggtgggtcta cagcggaagg gagggagcga 50  
aggtaggagg cagggcttgc ctactggcc accctcccaa cccaagagc 100  
ccagcccat ggtccccgcc gccggcgcg tgctgtgggt cctgctgctg 150

aatctgggtc cccgggcggc gggggoccaa ggctgaccc agactccgac 200  
cgaaatgcag cgggtcagtt tacgctttgg gggcccatg acccgagct 250  
accggagcac cgcccggaact ggttctcccc ggaagacaag gataatccta 300  
gaggacgaga atgatgccat ggccgaogcc gaccgcctgg ctggaccagc 350  
ggctgccgag ctcttgccg ccacgggtgc caccggcttt agccggctgt 400  
ccgccattaa cgaggaggat ggttcttcag aagaggggggt tgtgattaat 450  
gccggaaagg atagcaccag cagagagctt ccagtgcca ctccaatac 500  
agcggggagt tccagcacga ggtttatagc caatagtcag gagcctgaaa 550  
tcaggctgac ttcaagcctg ccgcgctccc ccgggaggtc tactgaggac 600  
ctgccaggct cgcaggccac cctgagccag tggtoacac ctgggtctac 650  
cccgagccgg tggccgtcac cctcaccac agccatgcca tctcctgagg 700  
atctgcccgt ggtgctgatg ccctggggcc cgtggcactg ccaactgcaag 750  
tcgggcacca tgagccggag ccggtctggg aagctgcacg gcctttccgg 800  
gcgccttcga gttggggcgc tgagccagct ccgcacggag cacaagcctt 850  
gcacctatca acaatgtccc tgcaaccgac ttogggaaga gtgccccctg 900  
gacacaagtc tctgtactga caccaactgt gcctctcaga gcaccaccag 950  
taccaggacc accactaccc ccttccccac catccacctc agaagcagtc 1000  
ccagcctgcc acccgccagc ccctgccag ccctggcttt ttggaaacgg 1050  
gtcaggattg gcctggagga tatttggaat agcctctctt cagtgttcac 1100  
agagatgcaa ccaatagaca gaaaccagag gtaatggcca ctccatccac 1150  
atgaggagat gtcagtatct caacctctct tgccctttca atcctagcac 1200  
ccactagata tttttagtac agaaaaacaa aactggaaaa caca 1245

<210> 297  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 297  
Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn  
1 5 10 15  
Leu Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro  
20 25 30  
Thr Glu Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr  
35 40 45  
Arg Ser Tyr Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr  
50 55 60  
Arg Ile Ile Leu Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp

65										70					75				
Arg	Leu	Ala	Gly	Pro	Ala	Ala	Ala	Glu	Leu	Leu	Leu	Ala	Ala	Thr	Val				
				80					85						90				
Ser	Thr	Gly	Phe	Ser	Arg	Ser	Ser	Ala	Ile	Asn	Glu	Glu	Asp	Gly					
				95					100					105					
Ser	Ser	Glu	Glu	Gly	Val	Val	Ile	Asn	Ala	Gly	Lys	Asp	Ser	Thr					
				110					115					120					
Ser	Arg	Glu	Leu	Pro	Ser	Ala	Thr	Pro	Asn	Thr	Ala	Gly	Ser	Ser					
				125					130					135					
Ser	Thr	Arg	Phe	Ile	Ala	Asn	Ser	Gln	Glu	Pro	Glu	Ile	Arg	Leu					
				140					145					150					
Thr	Ser	Ser	Leu	Pro	Arg	Ser	Pro	Gly	Arg	Ser	Thr	Glu	Asp	Leu					
				155					160					165					
Pro	Gly	Ser	Gln	Ala	Thr	Leu	Ser	Gln	Trp	Ser	Thr	Pro	Gly	Ser					
				170					175					180					
Thr	Pro	Ser	Arg	Trp	Pro	Ser	Pro	Ser	Pro	Thr	Ala	Met	Pro	Ser					
				185					190					195					
Pro	Glu	Asp	Leu	Arg	Leu	Val	Leu	Met	Pro	Trp	Gly	Pro	Trp	His					
				200					205					210					
Cys	His	Cys	Lys	Ser	Gly	Thr	Met	Ser	Arg	Ser	Arg	Ser	Gly	Lys					
				215					220					225					
Leu	His	Gly	Leu	Ser	Gly	Arg	Leu	Arg	Val	Gly	Ala	Leu	Ser	Gln					
				230					235					240					
Leu	Arg	Thr	Glu	His	Lys	Pro	Cys	Thr	Tyr	Gln	Gln	Cys	Pro	Cys					
				245					250					255					
Asn	Arg	Leu	Arg	Glu	Glu	Cys	Pro	Leu	Asp	Thr	Ser	Leu	Cys	Thr					
				260					265					270					
Asp	Thr	Asn	Cys	Ala	Ser	Gln	Ser	Thr	Thr	Ser	Thr	Arg	Thr	Thr					
				275					280					285					
Thr	Thr	Pro	Phe	Pro	Thr	Ile	His	Leu	Arg	Ser	Ser	Pro	Ser	Leu					
				290					295					300					
Pro	Pro	Ala	Ser	Pro	Cys	Pro	Ala	Leu	Ala	Phe	Trp	Lys	Arg	Val					
				305					310					315					
Arg	Ile	Gly	Leu	Glu	Asp	Ile	Trp	Asn	Ser	Leu	Ser	Ser	Val	Phe					
				320					325					330					
Thr	Glu	Met	Gln	Pro	Ile	Asp	Arg	Asn	Gln	Arg									
				335					340										

<210> 298  
 <211> 2692  
 <212> DNA  
 <213> Homo sapiens

<400> 298  
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 gtgggtcacc gttgggctct acctccagga aggtcacaaa gtgcctcagt 300  
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<210> 299  
 <211> 320  
 <212> PRT  
 <213> Homo sapiens

<400> 299  
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 35 40 45  
 Leu Asn His Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala  
 50 55 60  
 Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val  
 65 70 75

Thr	Val	Gly	Leu	Tyr	Leu	Gln	Glu	Gly	His	Lys	Val	Pro	Gln	Phe	
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His	Gly	Lys	Trp	Pro	Phe	Ser	Arg	Phe	Leu	Phe	Phe	Gln	Glu	Pro	
				95					100					105	
Ala	Ser	Ala	Val	Ala	Ser	Phe	Leu	Asn	Gly	Leu	Ala	Ser	Leu	Val	
				110					115					120	
Met	Leu	Cys	Arg	Tyr	Arg	Thr	Phe	Val	Pro	Ala	Ser	Ser	Pro	Met	
				125					130					135	
Tyr	His	Thr	Cys	Val	Ala	Phe	Ala	Trp	Val	Ser	Leu	Asn	Ala	Trp	
				140					145					150	
Phe	Trp	Ser	Thr	Val	Phe	His	Thr	Arg	Asp	Thr	Asp	Leu	Thr	Glu	
				155					160					165	
Lys	Met	Asp	Tyr	Phe	Cys	Ala	Ser	Thr	Val	Ile	Leu	His	Ser	Ile	
				170					175					180	
Tyr	Leu	Cys	Cys	Val	Arg	Thr	Val	Gly	Leu	Gln	His	Pro	Ala	Val	
				185					190					195	
Val	Ser	Ala	Phe	Arg	Ala	Leu	Leu	Leu	Leu	Met	Leu	Thr	Val	His	
				200					205					210	
Val	Ser	Tyr	Leu	Ser	Leu	Ile	Arg	Phe	Asp	Tyr	Gly	Tyr	Asn	Leu	
				215					220					225	
Val	Ala	Asn	Val	Ala	Ile	Gly	Leu	Val	Asn	Val	Val	Trp	Trp	Leu	
				230					235					240	
Ala	Trp	Cys	Leu	Trp	Asn	Gln	Arg	Arg	Leu	Pro	His	Val	Arg	Lys	
				245					250					255	
Cys	Val	Val	Val	Val	Leu	Leu	Leu	Gln	Gly	Leu	Ser	Leu	Leu	Glu	
				260					265					270	
Leu	Leu	Asp	Phe	Pro	Pro	Leu	Phe	Trp	Val	Leu	Asp	Ala	His	Ala	
				275					280					285	
Ile	Trp	His	Ile	Ser	Thr	Ile	Pro	Val	His	Val	Leu	Phe	Phe	Ser	
				290					295					300	
Phe	Leu	Glu	Asp	Asp	Ser	Leu	Tyr	Leu	Leu	Lys	Glu	Ser	Glu	Asp	
				305					310					315	
Lys	Phe	Lys	Leu	Asp											
				320											

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 <211> 1674  
 <212> DNA  
 <213> Homo sapiens

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 cctctgggca tgctgcttg gctgctgatg gccgcctgct tcaccttctg 150

cctcagtcacat cagaacctga aggagtttgc cctgaccaac ccagagaaga 200  
gcagcaccaa agaaacggag agaaaagaaa ccaaagccga ggaggagctg 250  
gatgcogaag tcctggaggt gttccaccgc acgcatgagt ggcaggccct 300  
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aatttgaaag gcaaaaggct ggatatcaac accaacacct acacatctca 450  
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gttcaaagga agacaaggca aggcaggctg aggtaaagcg gctcttccgc 550  
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gctccagttt ggaagagaag attgctgcgc tctttgatct tgaatattat 700  
gtccatcaga tggacaatgc gcaggacctg ctttctttg gtgggtcttc 750  
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<210> 301

<211> 461  
 <212> PRT  
 <213> Homo sapiens

<400> 301

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				20					25					30
Ser	His	Gln	Asn	Leu	Lys	Glu	Phe	Ala	Leu	Thr	Asn	Pro	Glu	Lys
				35					40					45
Ser	Ser	Thr	Lys	Glu	Thr	Glu	Arg	Lys	Glu	Thr	Lys	Ala	Glu	Glu
				50					55					60
Glu	Leu	Asp	Ala	Glu	Val	Leu	Glu	Val	Phe	His	Pro	Thr	His	Glu
				65					70					75
Trp	Gln	Ala	Leu	Gln	Pro	Gly	Gln	Ala	Val	Pro	Ala	Gly	Ser	His
				80					85					90
Val	Arg	Leu	Asn	Leu	Gln	Thr	Gly	Glu	Arg	Glu	Ala	Lys	Leu	Gln
				95					100					105
Tyr	Glu	Asp	Lys	Phe	Arg	Asn	Asn	Leu	Lys	Gly	Lys	Arg	Leu	Asp
				110					115					120
Ile	Asn	Thr	Asn	Thr	Tyr	Thr	Ser	Gln	Asp	Leu	Lys	Ser	Ala	Leu
				125					130					135
Ala	Lys	Phe	Lys	Glu	Gly	Ala	Glu	Met	Glu	Ser	Ser	Lys	Glu	Asp
				140					145					150
Lys	Ala	Arg	Gln	Ala	Glu	Val	Lys	Arg	Leu	Phe	Arg	Pro	Ile	Glu
				155					160					165
Glu	Leu	Lys	Lys	Asp	Phe	Asp	Glu	Leu	Asn	Val	Val	Ile	Glu	Thr
				170					175					180
Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser	Ser
				185					190					195
Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu
				200					205					210
Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe
				215					220					225
Gly	Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro
				230					235					240
Leu	Val	Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser
				245					250					255
Ser	Asn	Pro	Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu
				260					265					270
Gln	Lys	Leu	Leu	Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala
				275					280					285
Lys	Lys	Lys	Val	Leu	Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe

290	295	300
Pro Tyr Ala Gln Arg Gln Phe Leu Lys	Leu Gly Gly Leu Gln Val	
305	310	315
Leu Arg Thr Leu Val Gln Glu Lys Gly	Thr Glu Val Leu Ala Val	
320	325	330
Arg Val Val Thr Leu Leu Tyr Asp Leu	Val Thr Glu Lys Met Phe	
335	340	345
Ala Glu Glu Glu Ala Glu Leu Thr Gln	Glu Met Ser Pro Glu Lys	
350	355	360
Leu Gln Gln Tyr Arg Gln Val His Leu	Leu Pro Gly Leu Trp Glu	
365	370	375
Gln Gly Trp Cys Glu Ile Thr Ala His	Leu Leu Ala Leu Pro Glu	
380	385	390
His Asp Ala Arg Glu Lys Val Leu Gln	Thr Leu Gly Val Leu Leu	
395	400	405
Thr Thr Cys Arg Asp Arg Tyr Arg Gln	Asp Pro Gln Leu Gly Arg	
410	415	420
Thr Leu Ala Ser Leu Gln Ala Glu Tyr	Gln Val Leu Ala Ser Leu	
425	430	435
Glu Leu Gln Asp Gly Glu Asp Glu Gly	Tyr Phe Gln Glu Leu Leu	
440	445	450
Gly Ser Val Asn Ser Leu Leu Lys Glu	Leu Arg	
455	460	

<210> 302  
 <211> 2136  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
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ttaaccacca gcatccctcc tctccccaag gtgaagtgga gggtgctgtg 1850  
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2136

<210> 303  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 303

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Arg	Val	Ile	Ile	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	35	40	45	
Leu	Leu	Leu	Ala	Ser	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	50	55	60	
Asp	Arg	Ser	Asp	Ala	Arg	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	65	70	75	
Ala	Ala	Val	Ser	Val	Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	80	85	90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser	95	100	105	
Glu	Asp	Gly	Arg	Ser	Pro	Ile	Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val	110	115	120	
Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile	Ser	Gly	Val	Phe	Ser	Val	Ile	125	130	135	
Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro	Gly	Val	Val	Gly	Ile	His	140	145	150	
Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser	Ala	Phe	Leu	Thr	Ala	155	160	165	
Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val	Val	Phe	Phe	Asp	170	175	180	
Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu	Val	Val	Gly	185	190	195	
Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro	Trp	Tyr	200	205	210	
Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met	Gly	215	220	225	
Leu	Trp	Ala	Phe	Ile	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Ser	Ile	Gln	230	235	240	
Arg	Ser	Leu	Leu	Cys	Lys	Asp	245											

<210> 304  
 <211> 240  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> unsure  
<222> 108, 123, 126, 154, 198, 206, 217  
<223> unknown base

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ccttcggnat catcagtggg gtnttntctg ttatcaatat tttggctgat 150  
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cctganttca gccttnttga cagcagccat tatcctgctc 240

<210> 305  
<211> 378  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332  
<223> unknown base

<400> 305  
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ctgcttaaga aggcagatga ggggttagca tngctgagtg aggacggaag 150  
atcacccatt tccatccgcc agatggccta tgttnttggg ntttccttcg 200  
gtatcatcag tgggtgtttt tctgttatca atattttggg tgatgcantt 250  
gggccagggtg tggttgggat ccatggagan tcacctatt aattcctgaa 300  
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<210> 306  
<211> 655  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1, 22, 129, 133, 184  
<223> unknown base

<400> 306  
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gcgttgccac cccacgcgga ctccccagnt ggnngcgccct tcccatttgc 150  
ctgtcctggt caggccccca ccccccttcc cacntgacca gccatggggg 200  
ctgcggtgtt tttcggctgc actttcgtcg cgttcggccc ggccttcgcg 250

cttttcttga tcaactgtggc tggggaccog cttecggtta tcatcctggt 300  
 cgcaggggca tttttctggc tgggtctccct gctcctggcc tctgtggtct 350  
 ggttcatctt ggtccatgtg accgaccggt cagatgcccg gctccagta 400  
 ggccctcctga tttttggtgc tgetgtctct gtccttctac aggaggtgtt 450  
 ccgctttgcc tactacaagc tgcttaagaa ggcagatgag gggtttagcat 500  
 cgctgagtga ggacggaaga tcacccatct ccatccgcc gatggcctat 550  
 gtttctggtc tctccttcgg tatcatcagt ggtgtcttct ctgttatcaa 600  
 tattttggct gatgcacttg ggccaggtgt ggttgggatc catggagact 650  
 cacc 655

<210> 307  
 <211> 650  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 52, 89, 128  
 <223> unknown base

<400> 307  
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 cnttccccgg ggtctggggg tgacattgca ccgcgccnt cgtggggctcg 100  
 cgttgccacc ccacgcggac tccccagntg gcgcgccct ccatttggc 150  
 tgtcctggtc agggcccccac ccccttccc acctgaccag ccatgggggc 200  
 tgcggtgttt ttccggctgc actttcgtcg cgttcgggcc cggccttcgc 250  
 gcttttcttg atcaactgtg ctggggaccc gcttcgcgtt atcatcctgg 300  
 tcgcaggggc atttttctgg ctgggtctcc tgcctcctgg ctctgtggtc 350  
 tggttcatct tgggtccatgt gaccgaccgg tcagatgcc ggctccagta 400  
 cggcctcctg atttttggtg ctgctgtctc tgccttcta caggaggtgt 450  
 tccgctttgc ctactacaag ctgcttaaga aggcagatga ggggttagca 500  
 tcgctgagtg aggacggaag atcaccatc tccatccgcc agatggccta 550  
 tgtttctggt ctctccttcg gtatcatcag tgggtgtctt tctgttatca 600  
 atattttggc tgatgcactt gggccaggtg tggttgggat ccatggagac 650

<210> 308  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 308  
 gccccaggga gcagtgggtg gttataactc agggccggtg cccagagccc 50

aggaggaggc agtggccagg aaggcacagg cctgagaagt ctgcggtga 100  
 gctgggagca aatccccac cccctacctg ggggacaggg caagtgagac 150  
 ctgggtgaggg tggctcagca ggcagggaag gagaggtgtc tgtgcgtcct 200  
 gcacccacat ctttctctgt cccctccttg ccctgtctgg aggctgctag 250  
 actcctatct tctgaattct atagtgcctg ggtctcagcg cagtgccgat 300  
 ggtggcccggt ccttgtgggt cctctctacc tggggaaata aggtgcagcg 350  
 gccatggcta cagcaagacc cccctggatg tgggtgctct gtgctctgat 400  
 cacagccttg cttctggggg tcacagagca tgttctcgcc aacaatgatg 450  
 tttcctgtga ccacccctct aacaccgtgc cctctgggag caaccaggac 500  
 ctgggagctg gggccgggga agacgcccgg tcggatgaca gcagcagccg 550  
 catcatcaat ggatccgact gcgatatgca caccagccg tggcaggccg 600  
 cgctgttget aaggcccaac cagctctact gcggggcggt gttggtgcat 650  
 ccacagtggc tgctcacggc cgcccactgc aggaagaaag ttttcagagt 700  
 ccgtctcggc cactactccc tgtcaccagt ttatgaatct gggcagcaga 750  
 tgttccaggg ggtcaaatcc atccccacc ctggctactc ccaccctggc 800  
 cactctaacy acctcatgct catcaaactg aacagaagaa ttcgtccac 850  
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 caaagtgtct ggtgtctggc tgggggacaa ccaagagccc ccaagtgcac 950  
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 gtgcgaggat gcttaccga gacagataga tgacaccatg ttctgcgccg 1050  
 gtgacaaagc aggtagagac tcctgccagg gtgattcttg ggggcctgtg 1100  
 gtctgcaatg gctccctgca gggactcgtg tcctggggag attacccttg 1150  
 tgcccggccc aacagaccgg gtgtctacac gaacctctgc aagttcacca 1200  
 agtgatcca ggaaaccatc caggccaact cctgagtcac cccaggactc 1250  
 agcacaccgg catccccacc tgctgcaggg acagccctga cactccttcc 1300  
 agaccctcat tccttcccag agatgttgag aatgttcac tctccagccc 1350  
 ctgaccccat gtctcctgga ctgagggtct gcttccccca cattgggctg 1400  
 accgtgtctc tctagttgaa ccctgggaac aatttccaaa actgtccagg 1450  
 gcggggggttg cgtctcaatc tccctggggc actttcatcc tcaagctcag 1500  
 ggcccatccc ttctctgcag ctctgacca aatttagtcc cagaaataaa 1550  
 ctgagaagtg gaaaaaaaaa 1570

<210> 309

<211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 309

Met	Ala	Thr	Ala	Arg	Pro	Pro	Trp	Met	Trp	Val	Leu	Cys	Ala	Leu	1	5	10	15
Ile	Thr	Ala	Leu	Leu	Leu	Gly	Val	Thr	Glu	His	Val	Leu	Ala	Asn	20	25	30	
Asn	Asp	Val	Ser	Cys	Asp	His	Pro	Ser	Asn	Thr	Val	Pro	Ser	Gly	35	40	45	
Ser	Asn	Gln	Asp	Leu	Gly	Ala	Gly	Ala	Gly	Glu	Asp	Ala	Arg	Ser	50	55	60	
Asp	Asp	Ser	Ser	Ser	Arg	Ile	Ile	Asn	Gly	Ser	Asp	Cys	Asp	Met	65	70	75	
His	Thr	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Leu	Leu	Arg	Pro	Asn	Gln	80	85	90	
Leu	Tyr	Cys	Gly	Ala	Val	Leu	Val	His	Pro	Gln	Trp	Leu	Leu	Thr	95	100	105	
Ala	Ala	His	Cys	Arg	Lys	Lys	Val	Phe	Arg	Val	Arg	Leu	Gly	His	110	115	120	
Tyr	Ser	Leu	Ser	Pro	Val	Tyr	Glu	Ser	Gly	Gln	Gln	Met	Phe	Gln	125	130	135	
Gly	Val	Lys	Ser	Ile	Pro	His	Pro	Gly	Tyr	Ser	His	Pro	Gly	His	140	145	150	
Ser	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asn	Arg	Arg	Ile	Arg	Pro	155	160	165	
Thr	Lys	Asp	Val	Arg	Pro	Ile	Asn	Val	Ser	Ser	His	Cys	Pro	Ser	170	175	180	
Ala	Gly	Thr	Lys	Cys	Leu	Val	Ser	Gly	Trp	Gly	Thr	Thr	Lys	Ser	185	190	195	
Pro	Gln	Val	His	Phe	Pro	Lys	Val	Leu	Gln	Cys	Leu	Asn	Ile	Ser	200	205	210	
Val	Leu	Ser	Gln	Lys	Arg	Cys	Glu	Asp	Ala	Tyr	Pro	Arg	Gln	Ile	215	220	225	
Asp	Asp	Thr	Met	Phe	Cys	Ala	Gly	Asp	Lys	Ala	Gly	Arg	Asp	Ser	230	235	240	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Val	Val	Cys	Asn	Gly	Ser	Leu	245	250	255	
Gln	Gly	Leu	Val	Ser	Trp	Gly	Asp	Tyr	Pro	Cys	Ala	Arg	Pro	Asn	260	265	270	
Arg	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys	Lys	Phe	Thr	Lys	Trp	Ile	275	280	285	
Gln	Glu	Thr	Ile	Gln	Ala	Asn	Ser											

<210> 310  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 310  
 tcctgtgacc acccctctaa cacc 24

<210> 311  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 311  
 ctggaacatc tgctgcccag attc 24

<210> 312  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 312  
 gtcggatgac agcagcagcc gcatcatcaa tggatccgac tgcgatatgc 50

<210> 313  
 <211> 3010  
 <212> DNA  
 <213> Homo sapiens

<400> 313  
 atggtcaacg accggtggaa gaccatgggc ggcgctgccc aacttgagga 50  
 ccggccgcgc gacaagccgc agcggccgag ctgcggctac gtgctgtgca 100  
 ccgtgctgct ggccctggct gtgctgctgg ctgtagctgt caccggtgcc 150  
 gtgctcttcc tgaaccacgc ccacgcgccg ggcacggcgc cccacactgt 200  
 cgtcagcact ggggctgcca gcgccaacag cgccctggtc actgtggaaa 250  
 gggcggacag ctgcacctc agcatcctca ttgaccgcgc ctgccccgac 300  
 ctacccgaca gcttcgcacg cctggagagc gccaggcct cgggtgctgca 350  
 ggcgctgaca gagcaccagg ccagccacg gctggtgggc gaccaggagc 400  
 aggagctgct ggacacgctg gccgaccagc tgccccggct gctggcccga 450  
 gcctcagagc tgcagacgga gtgcatgggg ctgcggaagg ggcattggcac 500  
 gctgggccag ggcctcagcg ccctgcagag tgagcagggc cgcctcatcc 550

agcttctctc tgagagccag ggccacatgg ctcacctggt gaactccgtc 600  
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 caacaaggcc gaccttcaga gagcgctgc ccggggaacc cggccccggg 700  
 gctgtgccac tggctcccg ccccgagact gtctggacgt cctcctaagc 750  
 ggacagcagg acgatggcgt ctactctgtc tttcccaccc actaccggc 800  
 cggcttccag gtgtactgtg acatgcgcac ggacggcggc ggctggacgg 850  
 tgtttcagcg ccgggaggac ggctccgtga acttcttcgg gggctgggac 900  
 gcgtaccgag acggctttgg caggctcacc ggggagcact ggctagggct 950  
 caagaggatc cagccctga ccacacaggc tgccacgag ctgcaagtgg 1000  
 acctggagga ctttgagaat ggcacggcct atgcccgtc cgggagcttc 1050  
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 caacctcaat gggcagtacc tgcgcggtgc gcacgcctcc tatgccgacg 1300  
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 tttcgtgaat gttctccacc cactgtgcc tggcggaacc actctccagt 1500  
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 gggagaggcc gtgtgacctg gctctctgtc ccagtgcac caggatcatc 3000  
 acatgcgcag 3010

<210> 314  
 <211> 461  
 <212> PRT  
 <213> Homo sapiens

<400> 314  
 Met Val Asn Asp Arg Trp Lys Thr Met Gly Gly Ala Ala Gln Leu  
 1 5 10 15  
 Glu Asp Arg Pro Arg Asp Lys Pro Gln Arg Pro Ser Cys Gly Tyr  
 20 25 30  
 Val Leu Cys Thr Val Leu Leu Ala Leu Ala Val Leu Leu Ala Val  
 35 40 45  
 Ala Val Thr Gly Ala Val Leu Phe Leu Asn His Ala His Ala Pro  
 50 55 60  
 Gly Thr Ala Pro Pro Pro Val Val Ser Thr Gly Ala Ala Ser Ala  
 65 70 75  
 Asn Ser Ala Leu Val Thr Val Glu Arg Ala Asp Ser Ser His Leu  
 80 85 90  
 Ser Ile Leu Ile Asp Pro Arg Cys Pro Asp Leu Thr Asp Ser Phe  
 95 100 105

Ala	Arg	Leu	Glu	Ser	Ala	Gln	Ala	Ser	Val	Leu	Gln	Ala	Leu	Thr
				110					115					120
Glu	His	Gln	Ala	Gln	Pro	Arg	Leu	Val	Gly	Asp	Gln	Glu	Gln	Glu
				125					130					135
Leu	Leu	Asp	Thr	Leu	Ala	Asp	Gln	Leu	Pro	Arg	Leu	Leu	Ala	Arg
				140					145					150
Ala	Ser	Glu	Leu	Gln	Thr	Glu	Cys	Met	Gly	Leu	Arg	Lys	Gly	His
				155					160					165
Gly	Thr	Leu	Gly	Gln	Gly	Leu	Ser	Ala	Leu	Gln	Ser	Glu	Gln	Gly
				170					175					180
Arg	Leu	Ile	Gln	Leu	Leu	Ser	Glu	Ser	Gln	Gly	His	Met	Ala	His
				185					190					195
Leu	Val	Asn	Ser	Val	Ser	Asp	Ile	Leu	Asp	Ala	Leu	Gln	Arg	Asp
				200					205					210
Arg	Gly	Leu	Gly	Arg	Pro	Arg	Asn	Lys	Ala	Asp	Leu	Gln	Arg	Ala
				215					220					225
Pro	Ala	Arg	Gly	Thr	Arg	Pro	Arg	Gly	Cys	Ala	Thr	Gly	Ser	Arg
				230					235					240
Pro	Arg	Asp	Cys	Leu	Asp	Val	Leu	Leu	Ser	Gly	Gln	Gln	Asp	Asp
				245					250					255
Gly	Val	Tyr	Ser	Val	Phe	Pro	Thr	His	Tyr	Pro	Ala	Gly	Phe	Gln
				260					265					270
Val	Tyr	Cys	Asp	Met	Arg	Thr	Asp	Gly	Gly	Gly	Trp	Thr	Val	Phe
				275					280					285
Gln	Arg	Arg	Glu	Asp	Gly	Ser	Val	Asn	Phe	Phe	Arg	Gly	Trp	Asp
				290					295					300
Ala	Tyr	Arg	Asp	Gly	Phe	Gly	Arg	Leu	Thr	Gly	Glu	His	Trp	Leu
				305					310					315
Gly	Leu	Lys	Arg	Ile	His	Ala	Leu	Thr	Thr	Gln	Ala	Ala	Tyr	Glu
				320					325					330
Leu	His	Val	Asp	Leu	Glu	Asp	Phe	Glu	Asn	Gly	Thr	Ala	Tyr	Ala
				335					340					345
Arg	Tyr	Gly	Ser	Phe	Gly	Val	Gly	Leu	Phe	Ser	Val	Asp	Pro	Glu
				350					355					360
Glu	Asp	Gly	Tyr	Pro	Leu	Thr	Val	Ala	Asp	Tyr	Ser	Gly	Thr	Ala
				365					370					375
Gly	Asp	Ser	Leu	Leu	Lys	His	Ser	Gly	Met	Arg	Phe	Thr	Thr	Lys
				380					385					390
Asp	Arg	Asp	Ser	Asp	His	Ser	Glu	Asn	Asn	Cys	Ala	Ala	Phe	Tyr
				395					400					405
Arg	Gly	Ala	Trp	Trp	Tyr	Arg	Asn	Cys	His	Thr	Ser	Asn	Leu	Asn
				410					415					420

Gly	Gln	Tyr	Leu	Arg	Gly	Ala	His	Ala	Ser	Tyr	Ala	Asp	Gly	Val
				425					430					435
Glu	Trp	Ser	Ser	Trp	Thr	Gly	Trp	Gln	Tyr	Ser	Leu	Lys	Phe	Ser
				440					445					450
Glu	Met	Lys	Ile	Arg	Pro	Val	Arg	Glu	Asp	Arg				
				455					460					

<210> 315  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 315  
 cacacgtcca acctcaatgg gcag 24

<210> 316  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 316  
 gaccagcagg gcccaaggaca agg 23

<210> 317  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 317  
 gttctctgag atgaagatcc ggccggtccg ggagtaccgc ttag 44

<210> 318  
 <211> 1841  
 <212> DNA  
 <213> Homo sapiens

<400> 318  
 gcagtcagag acttcccctg cccctcgctg ggaaagaaca ttaggaatgc 50  
 ctttttagtgc cttgcttcct gaactagctc acagtagccc ggcggcccag 100  
 ggcaatccga ccacatttca ctctcaccgc tgtaggaatc cagatgcagg 150  
 ccaagtacag cagcacgagg gacatgctgg atgatgatgg ggacaccacc 200  
 atgagcctgc atttctcaagc ctctgccaca actcggcatc cagagccccg 250  
 gcgcacagag cacagggctc cctcttcaac gtggcgacca gtggccctga 300  
 ccctgctgac tttgtgcttg gtgctgctga tagggctggc agccctgggg 350  
 cttttgtttt ttcagtacta ccagctctcc aatactggtc aagacaccat 400

ttctcaaagt gaagaaagat taggaaatac gtccaagag ttgcaatctc 450  
 ttcaagtcca gaatataaag cttgcaggaa gtctgcagca tgtggctgaa 500  
 aaactctgtc gtgagctgta taacaaagct ggagcacaca ggtgcagccc 550  
 ttgtacagaa caatggaaat ggcattggaga caattgctac cagttctata 600  
 aagacagcaa aagttgggag gactgtaaat atttctgcct tagtgaaaac 650  
 tctaccatgc tgaagataaa caaacaagaa gacctggaat ttgccgcgtc 700  
 tcagagctac tctgagtttt tctactctta ttggacaggg cttttgcgcc 750  
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 gaactgttcc atattataat agatgtcacc agccaagaa gcagagactg 850  
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 catgtcccc ctgaaacatt aggcgaaggt gactgattcg ccctctgcaa 1000  
 ctacaaatag cagagtgagc caggcgggtc caaagcaagg gctagttgag 1050  
 acattgggaa atggaacata atcaggaaag actatctctc tgactagtac 1100  
 aaaatgggtt ctctgttttc ctgttcagga tcaccagcat ttctgagctt 1150  
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 caaccaacct cagaaacca taatgtcatc tgccttcttg gcttagagat 1250  
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 atgtcttctt tacacttggg ggaataagaa actttttgaa gtagaggaaa 1350  
 tacattgagg taacatcctt ttctctgaca gtcaagtagt ccatcagaaa 1400  
 ttggcagtca cttccagat tgtaccagca aatacacaag gaattctttt 1450  
 tgtttgtttc agttcatact agtcccttcc caatccatca gtaaagaccc 1500  
 catctgcctt gtccatgccg tttccaaca gggatgtcac ttgatatgag 1550  
 aatctcaaat ctcaatgcct tataagcatt ccttctgtg tccattaaga 1600  
 ctctgataat tgtctccctt ccataggaat ttctcccagg aaagaaatat 1650  
 atcccatct ccgtttcata tcagaactac cgtcccgat attcccttca 1700  
 gagagattaa agaccagaaa aaagtgagcc tcttcatctg cacctgtaat 1750  
 agtttcagtt cctattttct tccattgacc catatttata cctttcaggt 1800  
 actgaagatt taataataat aaatgtaaat actgtgaaaa a 1841

<210> 319  
 <211> 280  
 <212> PRT  
 <213> Homo sapiens

<400> 319

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				20					25					30
Arg	His	Pro	Glu	Pro	Arg	Arg	Thr	Glu	His	Arg	Ala	Pro	Ser	Ser
				35					40					45
Thr	Trp	Arg	Pro	Val	Ala	Leu	Thr	Leu	Leu	Thr	Leu	Cys	Leu	Val
				50					55					60
Leu	Leu	Ile	Gly	Leu	Ala	Ala	Leu	Gly	Leu	Leu	Phe	Phe	Gln	Tyr
				65					70					75
Tyr	Gln	Leu	Ser	Asn	Thr	Gly	Gln	Asp	Thr	Ile	Ser	Gln	Met	Glu
				80					85					90
Glu	Arg	Leu	Gly	Asn	Thr	Ser	Gln	Glu	Leu	Gln	Ser	Leu	Gln	Val
				95					100					105
Gln	Asn	Ile	Lys	Leu	Ala	Gly	Ser	Leu	Gln	His	Val	Ala	Glu	Lys
				110					115					120
Leu	Cys	Arg	Glu	Leu	Tyr	Asn	Lys	Ala	Gly	Ala	His	Arg	Cys	Ser
				125					130					135
Pro	Cys	Thr	Glu	Gln	Trp	Lys	Trp	His	Gly	Asp	Asn	Cys	Tyr	Gln
				140					145					150
Phe	Tyr	Lys	Asp	Ser	Lys	Ser	Trp	Glu	Asp	Cys	Lys	Tyr	Phe	Cys
				155					160					165
Leu	Ser	Glu	Asn	Ser	Thr	Met	Leu	Lys	Ile	Asn	Lys	Gln	Glu	Asp
				170					175					180
Leu	Glu	Phe	Ala	Ala	Ser	Gln	Ser	Tyr	Ser	Glu	Phe	Phe	Tyr	Ser
				185					190					195
Tyr	Trp	Thr	Gly	Leu	Leu	Arg	Pro	Asp	Ser	Gly	Lys	Ala	Trp	Leu
				200					205					210
Trp	Met	Asp	Gly	Thr	Pro	Phe	Thr	Ser	Glu	Leu	Phe	His	Ile	Ile
				215					220					225
Ile	Asp	Val	Thr	Ser	Pro	Arg	Ser	Arg	Asp	Cys	Val	Ala	Ile	Leu
				230					235					240
Asn	Gly	Met	Ile	Phe	Ser	Lys	Asp	Cys	Lys	Glu	Leu	Lys	Arg	Cys
				245					250					255
Val	Cys	Glu	Arg	Arg	Ala	Gly	Met	Val	Lys	Pro	Glu	Ser	Leu	His
				260					265					270
Val	Pro	Pro	Glu	Thr	Leu	Gly	Glu	Gly	Asp					
				275					280					

<210> 320

<211> 468

<212> DNA

<213> Homo sapiens

<220>  
 <221> unsure  
 <222> 59, 95, 149, 331, 364, 438, 446  
 <223> unknown base

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 aattttcacc gctgtaggaa tccagatgca ggccaagtac agcagcacga 50  
 gggacatgnt ggatgatgat gggacaccac catgagcctg cattntcaag 100  
 cttttgccac aattcggcat ccagagcccc ggcgcacaga gcacagggnt 150  
 cctttttcaa cgtggcgacc agtggccctg accctgctga ctttgtgctt 200  
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 ttaggaaata cgtcccaaga gttgcaattt nttcaagtcc agaataataa 350  
 gcttgacagga agtntgcagc atgtggctga aaaactctgt cgtgagctgt 400  
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 atacacacac cacttccc 468

<210> 321  
 <211> 23  
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<220>  
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<400> 321  
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<210> 322  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 322  
 catgctgacg acttcctgca agc 23

<210> 323  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 323  
 ccacacagtc tctgcttctt ggg 23

<210> 324  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 324  
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<210> 325  
<211> 2988  
<212> DNA  
<213> Homo sapiens

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gagggagcgg gcccgcccgc gggggccgag ccctccgat ccgccccctc 150  
cccgggtccc cccctcggga gactcctctg gctgctctgg gggttcgccg 200  
gggcccggga cccgcggtcc gggcgccatg cgggcatcgc tgetgctgtc 250  
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gctccctgcc ttttaataaac tggccaagtg tggaaaaa 2988

<210> 326

<211> 775

<212> PRT

<213> Homo sapiens

<400> 326

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Val	Ala	Val	Gly	Ile	Ser	Leu	Gly	Phe	Thr	Leu	Ser	Leu	Leu	Ser
			20						25					30

Val	Thr	Trp	Val	Glu	Glu	Pro	Cys	Gly	Pro	Gly	Pro	Pro	Gln	Pro
			35						40					45

Gly	Asp	Ser	Glu	Leu	Pro	Pro	Arg	Gly	Asn	Thr	Asn	Ala	Ala	Arg
			50						55					60

Arg	Pro	Asn	Ser	Val	Gln	Pro	Gly	Ala	Glu	Arg	Glu	Lys	Pro	Gly
			65						70					75

Ala	Gly	Glu	Gly	Ala	Gly	Glu	Asn	Trp	Glu	Pro	Arg	Val	Leu	Pro
			80						85					90

Tyr	His	Pro	Ala	Gln	Pro	Gly	Gln	Ala	Ala	Lys	Lys	Ala	Val	Arg
			95						100					105

Thr	Arg	Tyr	Ile	Ser	Thr	Glu	Leu	Gly	Ile	Arg	Gln	Arg	Leu	Leu
			110						115					120

Val	Ala	Val	Leu	Thr	Ser	Gln	Thr	Thr	Leu	Pro	Thr	Leu	Gly	Val
			125						130					135

Ala	Val	Asn	Arg	Thr	Leu	Gly	His	Arg	Leu	Glu	Arg	Val	Val	Phe
			140						145					150

Leu	Thr	Gly	Ala	Arg	Gly	Arg	Arg	Ala	Pro	Pro	Gly	Met	Ala	Val
			155						160					165

Val	Thr	Leu	Gly	Glu	Glu	Arg	Pro	Ile	Gly	His	Leu	His	Leu	Ala
			170						175					180

Leu	Arg	His	Leu	Leu	Glu	Gln	His	Gly	Asp	Asp	Phe	Asp	Trp	Phe
			185						190					195

Phe	Leu	Val	Pro	Asp	Thr	Thr	Tyr	Thr	Glu	Ala	His	Gly	Leu	Ala
			200						205					210

Arg	Leu	Thr	Gly	His	Leu	Ser	Leu	Ala	Ser	Ala	Ala	His	Leu	Tyr
			215						220					225

Leu	Gly	Arg	Pro	Gln	Asp	Phe	Ile	Gly	Gly	Glu	Pro	Thr	Pro	Gly
			230						235					240

Arg	Tyr	Cys	His	Gly	Gly	Phe	Gly	Val	Leu	Leu	Ser	Arg	Met	Leu
			245						250					255

Leu	Gln	Gln	Leu	Arg	Pro	His	Leu	Glu	Gly	Cys	Arg	Asn	Asp	Ile
			260						265					270

Val	Ser	Ala	Arg	Pro	Asp	Glu	Trp	Leu	Gly	Arg	Cys	Ile	Leu	Asp	275	280	285
Ala	Thr	Gly	Val	Gly	Cys	Thr	Gly	Asp	His	Glu	Gly	Val	His	Tyr	290	295	300
Ser	His	Leu	Glu	Leu	Ser	Pro	Gly	Glu	Pro	Val	Gln	Glu	Gly	Asp	305	310	315
Pro	His	Phe	Arg	Ser	Ala	Leu	Thr	Ala	His	Pro	Val	Arg	Asp	Pro	320	325	330
Val	His	Met	Tyr	Gln	Leu	His	Lys	Ala	Phe	Ala	Arg	Ala	Glu	Leu	335	340	345
Glu	Arg	Thr	Tyr	Gln	Glu	Ile	Gln	Glu	Leu	Gln	Trp	Glu	Ile	Gln	350	355	360
Asn	Thr	Ser	His	Leu	Ala	Val	Asp	Gly	Asp	Arg	Ala	Ala	Ala	Trp	365	370	375
Pro	Val	Gly	Ile	Pro	Ala	Pro	Ser	Arg	Pro	Ala	Ser	Arg	Phe	Glu	380	385	390
Val	Leu	Arg	Trp	Asp	Tyr	Phe	Thr	Glu	Gln	His	Ala	Phe	Ser	Cys	395	400	405
Ala	Asp	Gly	Ser	Pro	Arg	Cys	Pro	Leu	Arg	Gly	Ala	Asp	Arg	Ala	410	415	420
Asp	Val	Ala	Asp	Val	Leu	Gly	Thr	Ala	Leu	Glu	Glu	Leu	Asn	Arg	425	430	435
Arg	Tyr	His	Pro	Ala	Leu	Arg	Leu	Gln	Lys	Gln	Gln	Leu	Val	Asn	440	445	450
Gly	Tyr	Arg	Arg	Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	455	460	465
Asp	Leu	Gln	Leu	Glu	Ala	Leu	Thr	Pro	Gln	Gly	Gly	Arg	Arg	Pro	470	475	480
Leu	Thr	Arg	Arg	Val	Gln	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	485	490	495
Ile	Leu	Pro	Val	Pro	Tyr	Val	Thr	Glu	Ala	Ser	Arg	Leu	Thr	Val	500	505	510
Leu	Leu	Pro	Leu	Ala	Ala	Ala	Glu	Arg	Asp	Leu	Ala	Pro	Gly	Phe	515	520	525
Leu	Glu	Ala	Phe	Ala	Thr	Ala	Ala	Leu	Glu	Pro	Gly	Asp	Ala	Ala	530	535	540
Ala	Ala	Leu	Thr	Leu	Leu	Leu	Leu	Tyr	Glu	Pro	Arg	Gln	Ala	Gln	545	550	555
Arg	Val	Ala	His	Ala	Asp	Val	Phe	Ala	Pro	Val	Lys	Ala	His	Val	560	565	570
Ala	Glu	Leu	Glu	Arg	Arg	Phe	Pro	Gly	Ala	Arg	Val	Pro	Trp	Leu	575	580	585

Ser	Val	Gln	Thr	Ala	Ala	Pro	Ser	Pro	Leu	Arg	Leu	Met	Asp	Leu	590	595	600
Leu	Ser	Lys	Lys	His	Pro	Leu	Asp	Thr	Leu	Phe	Leu	Leu	Ala	Gly	605	610	615
Pro	Asp	Thr	Val	Leu	Thr	Pro	Asp	Phe	Leu	Asn	Arg	Cys	Arg	Met	620	625	630
His	Ala	Ile	Ser	Gly	Trp	Gln	Ala	Phe	Phe	Pro	Met	His	Phe	Gln	635	640	645
Ala	Phe	His	Pro	Gly	Val	Ala	Pro	Pro	Gln	Gly	Pro	Gly	Pro	Pro	650	655	660
Glu	Leu	Gly	Arg	Asp	Thr	Gly	Arg	Phe	Asp	Arg	Gln	Ala	Ala	Ser	665	670	675
Glu	Ala	Cys	Phe	Tyr	Asn	Ser	Asp	Tyr	Val	Ala	Ala	Arg	Gly	Arg	680	685	690
Leu	Ala	Ala	Ala	Ser	Glu	Gln	Glu	Glu	Glu	Leu	Leu	Glu	Ser	Leu	695	700	705
Asp	Val	Tyr	Glu	Leu	Phe	Leu	His	Phe	Ser	Ser	Leu	His	Val	Leu	710	715	720
Arg	Ala	Val	Glu	Pro	Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Ala	Gln	Thr	725	730	735
Cys	Ser	Ala	Arg	Leu	Ser	Glu	Asp	Leu	Tyr	His	Arg	Cys	Leu	Gln	740	745	750
Ser	Val	Leu	Glu	Gly	Leu	Gly	Ser	Arg	Thr	Gln	Leu	Ala	Met	Leu	755	760	765
Leu	Phe	Glu	Gln	Glu	Gln	Gly	Asn	Ser	Thr						770	775	

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 327  
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<210> 328  
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<220>  
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<400> 328  
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<210> 329  
 <211> 20

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<400> 329  
atggctcagt gtgcagacag 20

<210> 330  
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gcatgctgct ccgtgaagta gtcc 24

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<400> 331  
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<210> 332  
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<400> 332  
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<210> 333  
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<212> DNA  
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gctcccctag tggagaaaag gagtagctat tagccaattc ggcagggccc 150  
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tgctcttttc ccagtgggc gagggaaactc ggggcgattg gctgggaact 250  
gtatccaccc aaatgtcacc gatttcttcc tatgcaggaa atgagcagac 300  
ccatcaataa gaaattttct agcctggccg aaaatggttg gccccacgaa 350  
gccacgacaa ctggaggcaa agagggttgc tcaacgcccc gcctcattgg 400

aaaaccaa at cagatctggg acctatatag cgtggcggag gcggggcgat 450  
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 ccgcccccta gaccctgcag caccatctgt catggcggct gggctgtttg 550  
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 ctgcttcgac ccagcaaga tccagctgcc agaggatgag tgaccagttg 1000  
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<210> 334

<211> 153

<212> PRT

<213> Homo sapiens

<400> 334

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Ala	Ala	Ala	Thr	Arg	Gly	Leu	Pro	Ala	Ala	Arg	Val	Arg	Trp	Glu	20	25	30	
Ser	Ser	Phe	Ser	Arg	Thr	Val	Val	Ala	Pro	Ser	Ala	Val	Ala	Gly	35	40	45	
Lys	Arg	Pro	Pro	Glu	Pro	Thr	Thr	Pro	Trp	Gln	Glu	Asp	Pro	Glu	50	55	60	
Pro	Glu	Asp	Glu	Asn	Leu	Tyr	Glu	Lys	Asn	Pro	Asp	Ser	His	Gly	65	70	75	
Tyr	Asp	Lys	Asp	Pro	Val	Leu	Asp	Val	Trp	Asn	Met	Arg	Leu	Val	80	85	90	
Phe	Phe	Phe	Gly	Val	Ser	Ile	Ile	Leu	Val	Leu	Gly	Ser	Thr	Phe	95	100	105	
Val	Ala	Tyr	Leu	Pro	Asp	Tyr	Arg	Met	Lys	Glu	Trp	Ser	Arg	Arg	110	115	120	
Glu	Ala	Glu	Arg	Leu	Val	Lys	Tyr	Arg	Glu	Ala	Asn	Gly	Leu	Pro	125	130	135	
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Glu Asp Glu

<210> 335  
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<212> DNA  
<213> Homo sapiens

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aggactgtgg tcgccccgtc cgctgtggcg ggaaagcggc cccagaacc 150  
gaccacaccg tggcaagagg acccagaacc cgaggacgaa aacttgatg 200  
agaagaaccc agactcccat gggtatgaca aggaccccg tttggacgctc 250  
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tggcagcacc tttgtggcct atctgcctga ctacaggatg aaagagtgg 350  
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<210> 336  
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<223> Synthetic oligonucleotide probe

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<210> 337  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 337  
ggtgcttctt gagccccact tagc 24

<210> 338  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 338  
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<210> 339  
<211> 2162  
<212> DNA

<213> Homo sapiens

<400> 339

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tcatcaccac gctgccttcc ggggacgtag ccgccacatt ccagttccgc 150  
acgcgctggg attcggagct tcagcgggaa ggagtgtccc attacaggct 200  
ctttcccaaa gccctggggc agctgatctc caagtattct ctacggggagc 250  
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cccttcctgc aggcccatc aggtgcagag ctgtgggtct ggttocaaga 350  
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gagcacactg ctgtacaaca cccaccata ccgggccttc ccggtgctgc 1150  
tgctggacac cgtaccctgg tatctgggc tgtatgtgca caccctcacc 1200  
atcacctcca agggcaagga gaacaaacca agttacatcc actaccagcc 1250  
tgcccaggac cggctgcaac cccacctct ggagatgctg attcagctgc 1300  
cggccaactc agtcaccaag gtttccatcc agtttgagcg ggcgtgctg 1350  
aagtggaccg agtacacgcc agatcctaac catggcttct atgtcagccc 1400  
atctgtctc agcgccttg tgcccagcat ggtagcagcc aagccagtgg 1450  
actgggaaga gagtccctc ttaacagcc tgttccagct ctctgatggc 1500

tctaactact ttgtgcggt ctacacggag ccgctgctgg tgaacctgcc 1550  
gacaccggac ttcagcatgc cctacaacgt gatctgcctc acgtgcactg 1600  
tggtggccgt gtgctacggc tccttctaca atctcctcac ccgaaccttc 1650  
cacatcgagg agccccgcac aggtggcctg gccaaagcggc tggccaacct 1700  
tatccggcgc gcccgagggtg tccccccact ctgattcttg ccctttccag 1750  
cagctgcagc tgccgtttct ctctggggag gggagcccaa gggctgtttc 1800  
tgccacttgc tctcctcaga gttggctttt gaaccaaagt gccctggacc 1850  
aggtcagggc ctacagctgt gttgtccagt acaggagcca cgagccaaat 1900  
gtggcatttg aatttgaatt aacttagaaa ttcatttcct cacctgtagt 1950  
ggccacctct atattgaggt gctcaataag caaaagtggc cggtggtgc 2000  
tgtattggac agcacagaaa aagatttcca tcaccacaga aaggtcggct 2050  
ggcagcactg gccaaagtga tgggggtgtgc tacacagtgt atgtcactgt 2100  
gtagtggatg gagtttactg tttgtggaat aaaaacggct gtttccgtgg 2150  
aaaaaaaaaa aa 2162

<210> 340  
<211> 574  
<212> PRT  
<213> Homo sapiens

<400> 340  
Met Pro Leu Ala Leu Leu Val Leu Leu Leu Leu Gly Pro Gly Gly  
1 5 10 15  
Trp Cys Leu Ala Glu Pro Pro Arg Asp Ser Leu Arg Glu Glu Leu  
20 25 30  
Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala Thr Phe Gln  
35 40 45  
Phe Arg Thr Arg Trp Asp Ser Glu Leu Gln Arg Glu Gly Val Ser  
50 55 60  
His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser Lys  
65 70 75  
Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp  
80 85 90  
Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly  
95 100 105  
Ala Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp  
110 115 120  
Lys Ser Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys  
125 130 135  
Ala Ser Leu Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr  
140 145 150

Ala Ser Phe Lys	Pro Leu Gly Leu Ala	Asn Asp Thr Asp His Tyr	155	160	165
Phe Leu Arg Tyr	Ala Val Leu Pro Arg	Glu Val Val Cys Thr Glu	170	175	180
Asn Leu Thr Pro	Trp Lys Lys Leu Leu	Pro Cys Ser Ser Lys Ala	185	190	195
Gly Leu Ser Val	Leu Leu Lys Ala Asp	Arg Leu Phe His Thr Ser	200	205	210
Tyr His Ser Gln	Ala Val His Ile Arg	Pro Val Cys Arg Asn Ala	215	220	225
Arg Cys Thr Ser	Ile Ser Trp Glu Leu	Arg Gln Thr Leu Ser Val	230	235	240
Val Phe Asp Ala	Phe Ile Thr Gly Gln	Gly Lys Lys Asp Trp Ser	245	250	255
Leu Phe Arg Met	Phe Ser Arg Thr Leu	Thr Glu Pro Cys Pro Leu	260	265	270
Ala Ser Glu Ser	Arg Val Tyr Val Asp	Ile Thr Thr Tyr Asn Gln	275	280	285
Asp Asn Glu Thr	Leu Glu Val His Pro	Pro Pro Thr Thr Thr Tyr	290	295	300
Gln Asp Val Ile	Leu Gly Thr Arg Lys	Thr Tyr Ala Ile Tyr Asp	305	310	315
Leu Leu Asp Thr	Ala Met Ile Asn Asn	Ser Arg Asn Leu Asn Ile	320	325	330
Gln Leu Lys Trp	Lys Arg Pro Pro Glu	Asn Glu Ala Pro Pro Val	335	340	345
Pro Phe Leu His	Ala Gln Arg Tyr Val	Ser Gly Tyr Gly Leu Gln	350	355	360
Lys Gly Glu Leu	Ser Thr Leu Leu Tyr	Asn Thr His Pro Tyr Arg	365	370	375
Ala Phe Pro Val	Leu Leu Leu Asp Thr	Val Pro Trp Tyr Leu Arg	380	385	390
Leu Tyr Val His	Thr Leu Thr Ile Thr	Ser Lys Gly Lys Glu Asn	395	400	405
Lys Pro Ser Tyr	Ile His Tyr Gln Pro	Ala Gln Asp Arg Leu Gln	410	415	420
Pro His Leu Leu	Glu Met Leu Ile Gln	Leu Pro Ala Asn Ser Val	425	430	435
Thr Lys Val Ser	Ile Gln Phe Glu Arg	Ala Leu Leu Lys Trp Thr	440	445	450
Glu Tyr Thr Pro	Asp Pro Asn His Gly	Phe Tyr Val Ser Pro Ser	455	460	465

Val	Leu	Ser	Ala	Leu	Val	Pro	Ser	Met	Val	Ala	Ala	Lys	Pro	Val	
				470					475					480	
Asp	Trp	Glu	Glu	Ser	Pro	Leu	Phe	Asn	Ser	Leu	Phe	Pro	Val	Ser	
				485					490					495	
Asp	Gly	Ser	Asn	Tyr	Phe	Val	Arg	Leu	Tyr	Thr	Glu	Pro	Leu	Leu	
				500					505					510	
Val	Asn	Leu	Pro	Thr	Pro	Asp	Phe	Ser	Met	Pro	Tyr	Asn	Val	Ile	
				515					520					525	
Cys	Leu	Thr	Cys	Thr	Val	Val	Ala	Val	Cys	Tyr	Gly	Ser	Phe	Tyr	
				530					535					540	
Asn	Leu	Leu	Thr	Arg	Thr	Phe	His	Ile	Glu	Glu	Pro	Arg	Thr	Gly	
				545					550					555	
Gly	Leu	Ala	Lys	Arg	Leu	Ala	Asn	Leu	Ile	Arg	Arg	Ala	Arg	Gly	
				560					565					570	

Val Pro Pro Leu

<210> 341  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 341  
 tggacaccgt accctggtat ctgc 24

<210> 342  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic oligonucleotide probe

<400> 342  
 ccaactctga ggagagcaag tggc 24

<210> 343  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 343  
 tgtatgtgca caccctcacc atcacctcca agggcaagga gaac 44

<210> 344  
 <211> 762  
 <212> DNA  
 <213> Homo sapiens

<400> 344  
 caacatgggg tccagcagct tcttggtcct catggtgtct ctcgttcttg 50  
 tgacctgggt ggctgtggaa ggagttaaag agggatataga gaaagcaggg 100  
 gtttgcccag ctgacaacgt acgctgcttc aagtccgatc ctccccagtg 150  
 tcacacagac caggactgtc tgggggaaag gaagtgttgt tacctgcact 200  
 gtggcttcaa gtgtgtgatt cctgtgaagg aactggaaga aggaggaaac 250  
 aaggatgaag atgtgtcaag gccataccct gagccaggat gggaggccaa 300  
 gtgtccaggc tctcctcta ccagggtgcc tcagaaatga tgetgggtcc 350  
 tttctacctc tgggggtcac tctcacttgg cacctgcccc tgagggtcct 400  
 gagacttga atattggaaga agcaataccc aacccacca aagaaaacct 450  
 gagcttgaag tctttttccc caaaaagagg gaagagtcac aaaaagtcca 500  
 gaccccaggg acggtacttt cctctctac ctggtgctcc tccctaattgc 550  
 tcatgaatgg acccctcatg aatgaaacca gtgcccttat aagagacccc 600  
 aaagagctgc cttgcccttc tgcaatgtgt gatcacagct agaaggcact 650  
 gtcagagaag agaaactggt cctcaccaga tgetgaatct gctgggtgcct 700  
 tgatcttga cttcccagcc tctagaactg taagaaataa atatttgctg 750  
 ttataatcc aa 762

<210> 345  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 345  
 Met Gly Ser Ser Ser Phe Leu Val Leu Met Val Ser Leu Val Leu  
 1 5 10 15  
 Val Thr Leu Val Ala Val Glu Gly Val Lys Glu Gly Ile Glu Lys  
 20 25 30  
 Ala Gly Val Cys Pro Ala Asp Asn Val Arg Cys Phe Lys Ser Asp  
 35 40 45  
 Pro Pro Gln Cys His Thr Asp Gln Asp Cys Leu Gly Glu Arg Lys  
 50 55 60  
 Cys Cys Tyr Leu His Cys Gly Phe Lys Cys Val Ile Pro Val Lys  
 65 70 75  
 Glu Leu Glu Glu Gly Gly Asn Lys Asp Glu Asp Val Ser Arg Pro  
 80 85 90  
 Tyr Pro Glu Pro Gly Trp Glu Ala Lys Cys Pro Gly Ser Ser Ser  
 95 100 105  
 Thr Arg Cys Pro Gln Lys  
 110

<210> 346  
<211> 2528  
<212> DNA  
<213> Homo sapiens

<400> 346  
aaactcagca cttgccggag tggctcattg ttaagacaaa ggggtgtgcac 50  
ttcctggcca ggaaacctga gcggtgagac tcccagctgc ctacatcaag 100  
gccccaggac atgcagaacc ttcctctaga acccgaccca ccaccatgag 150  
gtcctgcctg tggagatgca ggcacctgag ccaaggcgtc cagtggctct 200  
tgcttctggc tgtcctggtc ttctttctct tcgccttgcc ctcttttatt 250  
aaggagcctc aaacaaagcc ttccaggcat caacgcacag agaacattaa 300  
agaaaggtct ctacagtccc tggcaaagcc taagtcccag gcacccacaa 350  
gggcgaggag gacaaccatc tatgcagagc cagcgccaga gaacaatgcc 400  
ctcaacacac aaaccagcc caaggcccac accaccggag acagaggaaa 450  
ggaggccaac caggcaccgc cggaggagca ggacaaggtg cccacacag 500  
cacagagggc agcatggaag agcccagaaa aagagaaaac catggtgaac 550  
acactgtcac ccagagggca agatgcaggg atggcctctg gcaggacaga 600  
ggcacaatca tggaagagcc aggacacaaa gacgacccaa ggaaatgggg 650  
gccagaccag gaagctgacg gcctccagga cgggtgtcaga gaagcaccag 700  
ggcaaagcgg caaccacagc caagacgctc attcccaaaa gtcagcacag 750  
aatgctggct cccacaggag cagtgtcaac aaggacgaga cagaaaggag 800  
tgaccacagc agtcatccca cctaaggaga agaaacctca ggccacccca 850  
ccccctgccc ctttcagag ccccacgacg cagagaaacc aaagactgaa 900  
ggccgccaac ttcaaactg agcctcggtg ggattttgag gaaaaatata 950  
gcttcgaaat aggaggcctt cagacgactt gccctgactc tgtgaagatc 1000  
aaagcctcca agtcgctgtg gctccagaaa ctctttctgc ccaacctcac 1050  
tctcttctg gactccagac acttcaacca gagtgagtgg gaccgcctgg 1100  
aacactttgc accacccttt ggcttcatgg agctcaacta ctcttggtg 1150  
cagaaggtcg tgacacgctt ccctccagtg cccagcagc agctgtctct 1200  
ggccagcctc cccgctggga gcctccggtg catcacctgt gccgtggtgg 1250  
gcaacggggg catcctgaac aactcccaca tgggccagga gatagacagt 1300  
cacgactacg tgttccgatt gagcggagct ctcattaaag gctacgaaca 1350  
ggatgtgggg actcggacat ccttctacgg ctttaccgcc ttctccctga 1400  
cccagtcact ccttatattg ggcaatcggg gtttcaagaa cgtgcctctt 1450

gggaaggacg tccgctactt gcacttcctg gaaggcaccc gggactatga 1500  
 gtggctggaa gcactgctta tgaatcagac ggtgatgtca aaaaaccttt 1550  
 tctggttcag gcacagaccc caggaagctt ttcgggaagc cctgcacatg 1600  
 gacaggtacc tgttgetgca cccagacttt ctccgataca tgaagaacag 1650  
 gtttctgagg tctaagaccc tggatgggtgc cactggagg atataccgcc 1700  
 ccaccactgg ggccctcctg ctgctcactg cccttcagct ctgtgaccag 1750  
 gtgagtgett atggcttcat cactgagggc catgagcgct tttctgatca 1800  
 ctactatgat acatcatgga agcggctgat cttttacata aaccatgact 1850  
 tcaagctgga gagagaagtc tggaagcggc tacacgatga agggataatc 1900  
 cggtgtacc agcgtcctgg tcccggaaact gccaaagcca agaactgacc 1950  
 ggggccaggg ctgccatggt ctccttgccct gctccaaggc acaggataca 2000  
 gtgggaatct tgagactctt tggccatttc ccatggctca gactaagctc 2050  
 caagcccttc aggagttcca agggaacact tgaaccatgg acaagactct 2100  
 ctcaagatgg caaatggcta attgaggttc tgaagttctt cagtacattg 2150  
 ctgtaggtcc tgaggccagg gatttttaat taaatggggg gatgggtggc 2200  
 caataccaca attcctgctg aaaaacactc ttccagtcca aaagcttctt 2250  
 gatacagaaa aaagagcctg gatttacaga aacatataga tctggtttga 2300  
 attccagatc gagtttacag ttgtgaaatc ttgaaggat tacttaactt 2350  
 cactacagat tgtctagaag acctttctag gagttatctg attctagaag 2400  
 ggtctatact tgtccttgctc ttttaagctat ttgacaactc taogtgttgt 2450  
 agaaaactga taataatata aatgattggt gtccatggaa aggcaaataa 2500  
 attttctaca gtgaaaaaaaa aaaaaaaaa 2528

<210> 347  
 <211> 600  
 <212> PRT  
 <213> Homo sapiens

<400> 347  
 Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val  
 1 5 10 15  
 Gln Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala  
 20 25 30  
 Leu Pro Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His  
 35 40 45  
 Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala  
 50 55 60  
 Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile

65					70					75				
Tyr	Ala	Glu	Pro	Ala	Pro	Glu	Asn	Asn	Ala	Leu	Asn	Thr	Gln	Thr
				80					85					90
Gln	Pro	Lys	Ala	His	Thr	Thr	Gly	Asp	Arg	Gly	Lys	Glu	Ala	Asn
				95					100					105
Gln	Ala	Pro	Pro	Glu	Glu	Gln	Asp	Lys	Val	Pro	His	Thr	Ala	Gln
				110					115					120
Arg	Ala	Ala	Trp	Lys	Ser	Pro	Glu	Lys	Glu	Lys	Thr	Met	Val	Asn
				125					130					135
Thr	Leu	Ser	Pro	Arg	Gly	Gln	Asp	Ala	Gly	Met	Ala	Ser	Gly	Arg
				140					145					150
Thr	Glu	Ala	Gln	Ser	Trp	Lys	Ser	Gln	Asp	Thr	Lys	Thr	Thr	Gln
				155					160					165
Gly	Asn	Gly	Gly	Gln	Thr	Arg	Lys	Leu	Thr	Ala	Ser	Arg	Thr	Val
				170					175					180
Ser	Glu	Lys	His	Gln	Gly	Lys	Ala	Ala	Thr	Thr	Ala	Lys	Thr	Leu
				185					190					195
Ile	Pro	Lys	Ser	Gln	His	Arg	Met	Leu	Ala	Pro	Thr	Gly	Ala	Val
				200					205					210
Ser	Thr	Arg	Thr	Arg	Gln	Lys	Gly	Val	Thr	Thr	Ala	Val	Ile	Pro
				215					220					225
Pro	Lys	Glu	Lys	Lys	Pro	Gln	Ala	Thr	Pro	Pro	Pro	Ala	Pro	Phe
				230					235					240
Gln	Ser	Pro	Thr	Thr	Gln	Arg	Asn	Gln	Arg	Leu	Lys	Ala	Ala	Asn
				245					250					255
Phe	Lys	Ser	Glu	Pro	Arg	Trp	Asp	Phe	Glu	Glu	Lys	Tyr	Ser	Phe
				260					265					270
Glu	Ile	Gly	Gly	Leu	Gln	Thr	Thr	Cys	Pro	Asp	Ser	Val	Lys	Ile
				275					280					285
Lys	Ala	Ser	Lys	Ser	Leu	Trp	Leu	Gln	Lys	Leu	Phe	Leu	Pro	Asn
				290					295					300
Leu	Thr	Leu	Phe	Leu	Asp	Ser	Arg	His	Phe	Asn	Gln	Ser	Glu	Trp
				305					310					315
Asp	Arg	Leu	Glu	His	Phe	Ala	Pro	Pro	Phe	Gly	Phe	Met	Glu	Leu
				320					325					330
Asn	Tyr	Ser	Leu	Val	Gln	Lys	Val	Val	Thr	Arg	Phe	Pro	Pro	Val
				335					340					345
Pro	Gln	Gln	Gln	Leu	Leu	Leu	Ala	Ser	Leu	Pro	Ala	Gly	Ser	Leu
				350					355					360
Arg	Cys	Ile	Thr	Cys	Ala	Val	Val	Gly	Asn	Gly	Gly	Ile	Leu	Asn
				365					370					375
Asn	Ser	His	Met	Gly	Gln	Glu	Ile	Asp	Ser	His	Asp	Tyr	Val	Phe

	380		385		390
Arg Leu Ser Gly	Ala Leu Ile Lys Gly	Tyr Glu Gln Asp Val Gly			
	395		400		405
Thr Arg Thr Ser	Phe Tyr Gly Phe Thr	Ala Phe Ser Leu Thr Gln			
	410		415		420
Ser Leu Leu Ile	Leu Gly Asn Arg Gly	Phe Lys Asn Val Pro Leu			
	425		430		435
Gly Lys Asp Val	Arg Tyr Leu His Phe	Leu Glu Gly Thr Arg Asp			
	440		445		450
Tyr Glu Trp Leu	Glu Ala Leu Leu Met	Asn Gln Thr Val Met Ser			
	455		460		465
Lys Asn Leu Phe	Trp Phe Arg His Arg	Pro Gln Glu Ala Phe Arg			
	470		475		480
Glu Ala Leu His	Met Asp Arg Tyr Leu	Leu Leu His Pro Asp Phe			
	485		490		495
Leu Arg Tyr Met	Lys Asn Arg Phe Leu	Arg Ser Lys Thr Leu Asp			
	500		505		510
Gly Ala His Trp	Arg Ile Tyr Arg Pro	Thr Thr Gly Ala Leu Leu			
	515		520		525
Leu Leu Thr Ala	Leu Gln Leu Cys Asp	Gln Val Ser Ala Tyr Gly			
	530		535		540
Phe Ile Thr Glu	Gly His Glu Arg Phe	Ser Asp His Tyr Tyr Asp			
	545		550		555
Thr Ser Trp Lys	Arg Leu Ile Phe Tyr	Ile Asn His Asp Phe Lys			
	560		565		570
Leu Glu Arg Glu	Val Trp Lys Arg Leu	His Asp Glu Gly Ile Ile			
	575		580		585
Arg Leu Tyr Gln	Arg Pro Gly Pro Gly	Thr Ala Lys Ala Lys Asn			
	590		595		600

<210> 348  
 <211> 496  
 <212> DNA  
 <213> Homo sapiens

<400> 348  
 cgatgcgcgg acccgggcac cccctcctcc tggggctgct gctgggtgctg 50  
 gggccttcgc cggagcagcg agtggaatt gttcctcgag atctgaggat 100  
 gaaggacaag tttctaaaac accttacagg ccctctttat tttagtccaa 150  
 agtgcagcaa acacttccat agactttatc acaacaccag agactgcacc 200  
 attcctgcat actataaaag atgcgccagg cttcttacct ggctggctgt 250  
 cagtccagtg tgcattgagg ataagtgagc agaccgtaca ggagcagcac 300  
 accaggagcc atgagaagtg ccttggaaac caacagggaa acagaactat 350

ctttatacac atccccctcat ggacaagaga tttatttttg cagacagact 400  
 cttccataag tcctttgagt tttgtatggt gttgacagtt tgcagatata 450  
 tattcgataa atcagtgtac ttgacagtgt tatctgtcac ttattt 496

<210> 349  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 349  
 Met Arg Gly Pro Gly His Pro Leu Leu Leu Gly Leu Leu Leu Val  
 1 5 10 15  
 Leu Gly Pro Ser Pro Glu Gln Arg Val Glu Ile Val Pro Arg Asp  
 20 25 30  
 Leu Arg Met Lys Asp Lys Phe Leu Lys His Leu Thr Gly Pro Leu  
 35 40 45  
 Tyr Phe Ser Pro Lys Cys Ser Lys His Phe His Arg Leu Tyr His  
 50 55 60  
 Asn Thr Arg Asp Cys Thr Ile Pro Ala Tyr Tyr Lys Arg Cys Ala  
 65 70 75  
 Arg Leu Leu Thr Arg Leu Ala Val Ser Pro Val Cys Met Glu Asp  
 80 85 90

Lys

<210> 350  
 <211> 1141  
 <212> DNA  
 <213> Homo sapiens

<400> 350  
 gggctggggc ccgccgcagc tccagctggc cggcttggtc ctgcgggtccc 50  
 ttctctggga ggcccgaccc cggccgcgcc cagccccac catgccaccc 100  
 gcggggctcc gccgggccgc gccgctcacc gcaatcgctc tgttggtgct 150  
 gggggctccc ctggtgctgg ccggcgagga ctgcctgtgg tacctggacc 200  
 ggaatggctc ctggcatccg gggtttaact gcgagttctt caccttctgc 250  
 tgccgggacct gctaccatcg gtactgctgc agggacctga ccttgcttat 300  
 caccgagagg cagcagaagc actgcctggc cttcagcccc aagaccatag 350  
 caggcatcgc ctgagctgtg atcctctttg ttgctgtggt tgccaccacc 400  
 atctgctgct tctctgttc ctgttgctac ctgtaccgcc ggcgccagca 450  
 gctccagagc ccatttgaag gccaggagat tccaatgaca ggcattccag 500  
 tgcagccagt ataccatac cccaggacc ccaaagctgg ccctgcaccc 550  
 ccacagcctg gttcatgta ccacactagt ggtcctgctc cccaatatcc 600

actctaccca gctgggcccc cagtctacaa ccctgcagct cctcctccct 650  
 atatgccacc acagccctct taccgggag cctgaggaac cagccatgtc 700  
 tctgctgccc cttcagtgat gccaaccttg ggagatgccc tcatactgta 750  
 cctgcatctg gtcctggggg tggcaggagt cctccagcca ccaggcccca 800  
 gaccaagcca agccctgggc cctactgggg acagagcccc aggggaagtgg 850  
 aacaggagct gaactagaac tatgaggggt tggggggagg gcttggaatt 900  
 atgggctatt ttactgggg gcaagggagg gagatgacag cctgggtcac 950  
 agtgcctgtt ttcaaatagt ccctctgctc ccaagatccc agccaggaag 1000  
 gctggggccc tactgtttgt cccctctggg ctgggggtggg gggagggagg 1050  
 aggttccgtc agcagctggc agtagccctc ctctctgggt gcccactgg 1100  
 ccacatctct ggcctgctag attaaagctg taaagacaaa a 1141

<210> 351

<211> 197

<212> PRT

<213> Homo sapiens

<400> 351

Met	Pro	Pro	Ala	Gly	Leu	Arg	Arg	Ala	Ala	Pro	Leu	Thr	Ala	Ile	1	5	10	15
Ala	Leu	Leu	Val	Leu	Gly	Ala	Pro	Leu	Val	Leu	Ala	Gly	Glu	Asp	20	25	30	
Cys	Leu	Trp	Tyr	Leu	Asp	Arg	Asn	Gly	Ser	Trp	His	Pro	Gly	Phe	35	40	45	
Asn	Cys	Glu	Phe	Phe	Thr	Phe	Cys	Cys	Gly	Thr	Cys	Tyr	His	Arg	50	55	60	
Tyr	Cys	Cys	Arg	Asp	Leu	Thr	Leu	Leu	Ile	Thr	Glu	Arg	Gln	Gln	65	70	75	
Lys	His	Cys	Leu	Ala	Phe	Ser	Pro	Lys	Thr	Ile	Ala	Gly	Ile	Ala	80	85	90	
Ser	Ala	Val	Ile	Leu	Phe	Val	Ala	Val	Val	Ala	Thr	Thr	Ile	Cys	95	100	105	
Cys	Phe	Leu	Cys	Ser	Cys	Cys	Tyr	Leu	Tyr	Arg	Arg	Arg	Gln	Gln	110	115	120	
Leu	Gln	Ser	Pro	Phe	Glu	Gly	Gln	Glu	Ile	Pro	Met	Thr	Gly	Ile	125	130	135	
Pro	Val	Gln	Pro	Val	Tyr	Pro	Tyr	Pro	Gln	Asp	Pro	Lys	Ala	Gly	140	145	150	
Pro	Ala	Pro	Pro	Gln	Pro	Gly	Phe	Met	Tyr	Pro	Pro	Ser	Gly	Pro	155	160	165	
Ala	Pro	Gln	Tyr	Pro	Leu	Tyr	Pro	Ala	Gly	Pro	Pro	Val	Tyr	Asn	170	175	180	

Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro Ser Tyr Pro  
 185 190 195

Gly Ala

<210> 352  
 <211> 3226  
 <212> DNA  
 <213> Homo sapiens

<400> 352  
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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Pro Phe Pro Trp Asn Lys Ile Arg Leu Pro Glu Tyr Val Ile Pro  
 50 55 60  
 Val His Tyr Asp Leu Leu Ile His Ala Asn Leu Thr Thr Leu Thr  
 65 70 75  
 Phe Trp Gly Thr Thr Lys Val Glu Ile Thr Ala Ser Gln Pro Thr  
 80 85 90  
 Ser Thr Ile Ile Leu His Ser His His Leu Gln Ile Ser Arg Ala  
 95 100 105  
 Thr Leu Arg Lys Gly Ala Gly Glu Arg Leu Ser Glu Glu Pro Leu  
 110 115 120  
 Gln Val Leu Glu His Pro Pro Gln Glu Gln Ile Ala Leu Leu Ala  
 125 130 135  
 Pro Glu Pro Leu Leu Val Gly Leu Pro Tyr Thr Val Val Ile His  
 140 145 150  
 Tyr Ala Gly Asn Leu Ser Glu Thr Phe His Gly Phe Tyr Lys Ser  
 155 160 165  
 Thr Tyr Arg Thr Lys Glu Gly Glu Leu Arg Ile Leu Ala Ser Thr  
 170 175 180  
 Gln Phe Glu Pro Thr Ala Ala Arg Met Ala Phe Pro Cys Phe Asp  
 185 190 195  
 Glu Pro Ala Phe Lys Ala Ser Phe Ser Ile Lys Ile Arg Arg Glu  
 200 205 210  
 Pro Arg His Leu Ala Ile Ser Asn Met Pro Leu Val Lys Ser Val

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Lys	Met	Ser	Thr	Tyr	Leu	Val	Ala	Phe	Ile	Ile	Ser	Asp	Phe	Glu
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Ser	Val	Ser	Lys	Ile	Thr	Lys	Ser	Gly	Val	Lys	Val	Ser	Val	Tyr
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Ala	Val	Pro	Asp	Lys	Ile	Asn	Gln	Ala	Asp	Tyr	Ala	Leu	Asp	Ala
				275					280					285
Ala	Val	Thr	Leu	Leu	Glu	Phe	Tyr	Glu	Asp	Tyr	Phe	Ser	Ile	Pro
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Tyr	Pro	Leu	Pro	Lys	Gln	Asp	Leu	Ala	Ala	Ile	Pro	Asp	Phe	Gln
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Ser	Gly	Ala	Met	Glu	Asn	Trp	Gly	Leu	Thr	Thr	Tyr	Arg	Glu	Ser
				320					325					330
Ala	Leu	Leu	Phe	Asp	Ala	Glu	Lys	Ser	Ser	Ala	Ser	Ser	Lys	Leu
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Gly	Ile	Thr	Val	Thr	Val	Ala	His	Glu	Leu	Ala	His	Gln	Trp	Phe
				350					355					360
Gly	Asn	Leu	Val	Thr	Met	Glu	Trp	Trp	Asn	Asp	Leu	Trp	Leu	Asn
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Glu	Gly	Phe	Ala	Lys	Phe	Met	Glu	Phe	Val	Ser	Val	Ser	Val	Thr
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His	Pro	Glu	Leu	Lys	Val	Gly	Asp	Tyr	Phe	Phe	Gly	Lys	Cys	Phe
				395					400					405
Asp	Ala	Met	Glu	Val	Asp	Ala	Leu	Asn	Ser	Ser	His	Pro	Val	Ser
				410					415					420
Thr	Pro	Val	Glu	Asn	Pro	Ala	Gln	Ile	Arg	Glu	Met	Phe	Asp	Asp
				425					430					435
Val	Ser	Tyr	Asp	Lys	Gly	Ala	Cys	Ile	Leu	Asn	Met	Leu	Arg	Glu
				440					445					450
Tyr	Leu	Ser	Ala	Asp	Ala	Phe	Lys	Ser	Gly	Ile	Val	Gln	Tyr	Leu
				455					460					465
Gln	Lys	His	Ser	Tyr	Lys	Asn	Thr	Lys	Asn	Glu	Asp	Leu	Trp	Asp
				470					475					480
Ser	Met	Ala	Ser	Ile	Cys	Pro	Thr	Asp	Gly	Val	Lys	Gly	Met	Asp
				485					490					495
Gly	Phe	Cys	Ser	Arg	Ser	Gln	His	Ser	Ser	Ser	Ser	Ser	His	Trp
				500					505					510
His	Gln	Glu	Gly	Val	Asp	Val	Lys	Thr	Met	Met	Asn	Thr	Trp	Thr
				515					520					525
Leu	Gln	Arg	Gly	Phe	Pro	Leu	Ile	Thr	Ile	Thr	Val	Arg	Gly	Arg

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Asn	Val	His	Met	Lys	Gln	Glu	His	Tyr	Met	Val	Lys	Gly	Ser	Asp	Gly				
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Ala	Pro	Asp	Thr	Gly	Tyr	Leu	Trp	His	Val	Pro	Leu	Thr	Phe	Ile					
				560					565					570					
Thr	Ser	Lys	Ser	Asn	Met	Val	His	Arg	Phe	Leu	Leu	Lys	Thr	Lys					
				575					580					585					
Thr	Asp	Val	Leu	Ile	Leu	Pro	Glu	Glu	Val	Glu	Trp	Ile	Lys	Phe					
				590					595					600					
Asn	Val	Gly	Met	Asn	Gly	Tyr	Tyr	Ile	Val	His	Tyr	Glu	Asp	Asp					
				605					610					615					
Gly	Trp	Asp	Ser	Leu	Thr	Gly	Leu	Leu	Lys	Gly	Thr	His	Thr	Ala					
				620					625					630					
Val	Ser	Ser	Asn	Asp	Arg	Ala	Ser	Leu	Ile	Asn	Asn	Ala	Phe	Gln					
				635					640					645					
Leu	Val	Ser	Ile	Gly	Lys	Leu	Ser	Ile	Glu	Lys	Ala	Leu	Asp	Leu					
				650					655					660					
Ser	Leu	Tyr	Leu	Lys	His	Glu	Thr	Glu	Ile	Met	Pro	Val	Phe	Gln					
				665					670					675					
Gly	Leu	Asn	Glu	Leu	Ile	Pro	Met	Tyr	Lys	Leu	Met	Glu	Lys	Arg					
				680					685					690					
Asp	Met	Asn	Glu	Val	Glu	Thr	Gln	Phe	Lys	Ala	Phe	Leu	Ile	Arg					
				695					700					705					
Leu	Leu	Arg	Asp	Leu	Ile	Asp	Lys	Gln	Thr	Trp	Thr	Asp	Glu	Gly					
				710					715					720					
Ser	Val	Ser	Glu	Gln	Met	Leu	Arg	Ser	Glu	Leu	Leu	Leu	Leu	Ala					
				725					730					735					
Cys	Val	His	Asn	Tyr	Gln	Pro	Cys	Val	Gln	Arg	Ala	Glu	Gly	Tyr					
				740					745					750					
Phe	Arg	Lys	Trp	Lys	Glu	Ser	Asn	Gly	Asn	Leu	Ser	Leu	Pro	Val					
				755					760					765					
Asp	Val	Thr	Leu	Ala	Val	Phe	Ala	Val	Gly	Ala	Gln	Ser	Thr	Glu					
				770					775					780					
Gly	Trp	Asp	Phe	Leu	Tyr	Ser	Lys	Tyr	Gln	Phe	Ser	Leu	Ser	Ser					
				785					790					795					
Thr	Glu	Lys	Ser	Gln	Ile	Glu	Phe	Ala	Leu	Cys	Arg	Thr	Gln	Asn					
				800					805					810					
Lys	Glu	Lys	Leu	Gln	Trp	Leu	Leu	Asp	Glu	Ser	Phe	Lys	Gly	Asp					
				815					820					825					
Lys	Ile	Lys	Thr	Gln	Glu	Phe	Pro	Gln	Ile	Leu	Thr	Leu	Ile	Gly					
				830					835					840					
Arg	Asn	Pro	Val	Gly	Tyr	Pro	Leu	Ala	Trp	Gln	Phe	Leu	Arg	Lys					

	845		850		855
Asn Trp Asn Lys	Leu Val Gln Lys Phe	Glu Leu Gly Ser Ser Ser			
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Ile Ala His Met	Val Met Gly Thr Thr	Asn Gln Phe Ser Thr Arg			
	875		880		885
Thr Arg Leu Glu	Glu Val Lys Gly Phe	Phe Ser Ser Leu Lys Glu			
	890		895		900
Asn Gly Ser Gln	Leu Arg Cys Val Gln	Gln Thr Ile Glu Thr Ile			
	905		910		915
Glu Glu Asn Ile	Gly Trp Met Asp Lys	Asn Phe Asp Lys Ile Arg			
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 <212> DNA  
 <213> Homo sapiens

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 <211> 437  
 <212> PRT  
 <213> Homo sapiens

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 His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys  
 35 40 45  
 Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met  
 50 55 60  
 Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly  
 65 70 75  
 Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg  
 80 85 90  
 Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg  
 95 100 105  
 Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp  
 110 115 120  
 Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val  
 125 130 135  
 Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile  
 140 145 150  
 Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu

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Pro	Gln	Pro	Gly	Cys	Asn	Leu	Leu	Asn	Gly	Thr	Gln	Glu	Ile	Gly					
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Pro	Val	Gly	Met	Thr	Glu	Asn	Cys	Asn	Arg	Lys	Asp	Phe	Leu	Thr					
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Cys	His	Arg	Gly	Thr	Thr	Ile	Met	Thr	His	Gly	Asn	Leu	Ala	Gln					
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Glu	Pro	Thr	Asp	Trp	Thr	Thr	Ser	Asn	Thr	Glu	Met	Cys	Glu	Val					
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Gly	Gln	Val	Cys	Gln	Glu	Thr	Leu	Leu	Leu	Ile	Asp	Val	Gly	Leu					
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Thr	Ser	Thr	Leu	Val	Gly	Thr	Lys	Gly	Cys	Ser	Thr	Val	Gly	Ala					
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Gln	Asn	Ser	Gln	Lys	Thr	Thr	Ile	His	Ser	Ala	Pro	Pro	Gly	Val					
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Leu	Val	Ala	Ser	Tyr	Thr	His	Phe	Cys	Ser	Ser	Asp	Leu	Cys	Asn					
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Ser	Ala	Ser	Ser	Ser	Ser	Val	Leu	Leu	Asn	Ser	Leu	Pro	Pro	Gln					
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Arg	Gly	Ala	Thr	His	Cys	Tyr	Asp	Gly	Tyr	Ile	His	Leu	Ser	Gly					
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Gly	Gly	Leu	Ser	Thr	Lys	Met	Ser	Ile	Gln	Gly	Cys	Val	Ala	Gln					
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Pro	Ser	Ser	Phe	Leu	Leu	Asn	His	Thr	Arg	Gln	Ile	Gly	Ile	Phe					
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Ser	Ala	Arg	Glu	Lys	Arg	Asp	Val	Gln	Pro	Pro	Ala	Ser	Gln	His					
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Glu	Gly	Gly	Gly	Ala	Glu	Gly	Leu	Glu	Ser	Leu	Thr	Trp	Gly	Val					
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<210> 356  
 <211> 1238  
 <212> DNA  
 <213> Homo sapiens

<400> 356

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<210> 357

<211> 271

<212> PRT

<213> Homo sapiens

<400> 357

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Phe	Leu	Ser	Leu	Leu	Pro	Ser	Gly	His	Pro	Gln	Pro	Ala	Gly	Asp
			20					25					30	

Asp	Ala	Cys	Ser	Val	Gln	Ile	Leu	Val	Pro	Gly	Leu	Lys	Gly	Asp	35	40	45
Ala	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Ala	Pro	Gly	Arg	Pro	Gly	Arg	50	55	60
Val	Gly	Pro	Thr	Gly	Glu	Lys	Gly	Asp	Met	Gly	Asp	Lys	Gly	Gln	65	70	75
Lys	Gly	Ser	Val	Gly	Arg	His	Gly	Lys	Ile	Gly	Pro	Ile	Gly	Ser	80	85	90
Lys	Gly	Glu	Lys	Gly	Asp	Ser	Gly	Asp	Ile	Gly	Pro	Pro	Gly	Pro	95	100	105
Asn	Gly	Glu	Pro	Gly	Leu	Pro	Cys	Glu	Cys	Ser	Gln	Leu	Arg	Lys	110	115	120
Ala	Ile	Gly	Glu	Met	Asp	Asn	Gln	Val	Ser	Gln	Leu	Thr	Ser	Glu	125	130	135
Leu	Lys	Phe	Ile	Lys	Asn	Ala	Val	Ala	Gly	Val	Arg	Glu	Thr	Glu	140	145	150
Ser	Lys	Ile	Tyr	Leu	Leu	Val	Lys	Glu	Glu	Lys	Arg	Tyr	Ala	Asp	155	160	165
Ala	Gln	Leu	Ser	Cys	Gln	Gly	Arg	Gly	Gly	Thr	Leu	Ser	Met	Pro	170	175	180
Lys	Asp	Glu	Ala	Ala	Asn	Gly	Leu	Met	Ala	Ala	Tyr	Leu	Ala	Gln	185	190	195
Ala	Gly	Leu	Ala	Arg	Val	Phe	Ile	Gly	Ile	Asn	Asp	Leu	Glu	Lys	200	205	210
Glu	Gly	Ala	Phe	Val	Tyr	Ser	Asp	His	Ser	Pro	Met	Arg	Thr	Phe	215	220	225
Asn	Lys	Trp	Arg	Ser	Gly	Glu	Pro	Asn	Asn	Ala	Tyr	Asp	Glu	Glu	230	235	240
Asp	Cys	Val	Glu	Met	Val	Ala	Ser	Gly	Gly	Trp	Asn	Asp	Val	Ala	245	250	255
Cys	His	Thr	Thr	Met	Tyr	Phe	Met	Cys	Glu	Phe	Asp	Lys	Glu	Asn	260	265	270

Met

<210> 358  
 <211> 972  
 <212> DNA  
 <213> Homo sapiens

<400> 358  
 agtgactgca gccttcctag atccccctcca ctcggtttct ctctttgcag 50  
 gagcaccggc agcaccagtg tgtgagggga gcaggcagcg gtcctagcca 100  
 gttccttgat cctgccagac caccagccc ccggcacaga gctgctccac 150

aggcaccatg aggatcatgc tgctattcac agccatcctg gccttcagcc 200  
 tagctcagag ctttggggct gtctgtaagg agccacagga ggagggtggtt 250  
 cctggcgggg gccgcagcaa gagggatcca gatctctacc agctgctcca 300  
 gagactcttc aaaagccact catctctgga gggattgctc aaagccctga 350  
 gccaggctag cacagatcct aaggaatcaa catctcccga gaaacgtgac 400  
 atgcatgact tctttgtggg acttatgggc aagaggagcg tccagccaga 450  
 gggaaagaca ggacctttct taccttcagt gagggttcct cggccccctc 500  
 atcccaatca gcttggatcc acaggaaagt cttccctggg aacagaggag 550  
 cagagacctt tataagactc tctacggat gtgaatcaag agaacgtccc 600  
 cagctttggc atcctcaagt atccccgag agcagaatag gtactccact 650  
 tccggactcc tggactgcat taggaagacc tctttccctg tcccaatccc 700  
 cagggtgcga cgctcctggt accctttctc ttccctgttc ttgtaacatt 750  
 cttgtgcttt gaactccttct ccactctttc tacctgacct tgggtggaa 800  
 actgcatagt gaatatcccc aaccccaatg ggcattgact gtagaatacc 850  
 ctagagttcc tgtagtgtcc tacattaata atataatgtc tctctctatt 900  
 cctcaacaat aaaggatttt tgcatatgaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aa 972

<210> 359  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 359  
 Met Arg Ile Met Leu Leu Phe Thr Ala Ile Leu Ala Phe Ser Leu  
 1 5 10 15  
 Ala Gln Ser Phe Gly Ala Val Cys Lys Glu Pro Gln Glu Glu Val  
 20 25 30  
 Val Pro Gly Gly Gly Arg Ser Lys Arg Asp Pro Asp Leu Tyr Gln  
 35 40 45  
 Leu Leu Gln Arg Leu Phe Lys Ser His Ser Ser Leu Glu Gly Leu  
 50 55 60  
 Leu Lys Ala Leu Ser Gln Ala Ser Thr Asp Pro Lys Glu Ser Thr  
 65 70 75  
 Ser Pro Glu Lys Arg Asp Met His Asp Phe Phe Val Gly Leu Met  
 80 85 90  
 Gly Lys Arg Ser Val Gln Pro Glu Gly Lys Thr Gly Pro Phe Leu  
 95 100 105  
 Pro Ser Val Arg Val Pro Arg Pro Leu His Pro Asn Gln Leu Gly  
 110 115 120

Ser	Thr	Gly	Lys	Ser	Ser	Leu	Gly	Thr	Glu	Glu	Gln	Arg	Pro	Leu
				125					130					135

<210> 360  
 <211> 1738  
 <212> DNA  
 <213> Homo sapiens

<400> 360  
 gggcgtctcc ggctgctcct attgagctgt ctgctcgtgt tgcccgtgt 50  
 goctgctgtg cccgcgtgt cgcgcgtgt accgcgtctg ctggacgcgg 100  
 gagacgccag cgagctggtg attggagccc tgccgagagc tcaagcgccc 150  
 agctctgccc caggagccca ggctgccccg tgagtcccat agttgctgca 200  
 ggagtggagc catgagctgc gtccctgggtg gtgtcatccc cttggggctg 250  
 ctgttctctg tctgcggatc ccaaggctac ctccctgcca acgtcactct 300  
 cttagaggag ctgctcagca aataccagca caacgagtct cactcccggg 350  
 tccgcagagc catccccagg gaggacaagg aggagatcct catgctgcac 400  
 aacaagcttc ggggccaggt gcagcctcag gcctccaaca tggagtacat 450  
 ggtgagcgcc ggctccggcc gcagaggctg gcaccggggg tggggcctgg 500  
 gccaccagcc tgctctgttc ccagccagc tctgttcccc agccagtgcg 550  
 tgtgatggct ggctcagggt ctccctctggc aggggaggat cccggctctg 600  
 ttctgttttg tttgtttgtt ttgagacagg gtctcactct gccactgacg 650  
 ctggagtgca atggcacaat cgtcatgccc tgaaacctta gactcccggg 700  
 gttaagcgat cctgcttcag cctcccaagt agctggaact acaggcatgc 750  
 accatggtgc ccagctagat tttaaatatt ttgtggagat gggggtcttg 800  
 ctacgttgcc caggctggtc ttgaactcct aggcctcaagc aatcctcctg 850  
 cctcagcctc tcaaagtgtc aggattatag gcatgagtca ccctgtctgg 900  
 ctctggtctt gttcttaaca ttctgccaaa acaacacacg tgggttccct 950  
 gtgcagagcc tgccctcgtt ccttcattgt actcttggtg gctccactgg 1000  
 gaacacagct ctacgccttt ccacactgga ggcagagtgg ggaggggccc 1050  
 agggctgggc tttgctgatg ctgatctcag ctgtgccaca cgctagctgc 1100  
 accaccctga cttctcctta gcccggtgtg gcctcacttt ccacttgag 1150  
 agtccttcct cgcgtgggtg ccatgactgt gagataagtc gaggctgtga 1200  
 agggcccggc acagactgac ctgcctcccc aaccctagg ctttgctaac 1250  
 cgggaaagga gctaacggtg acagaagaca gccaaagtc accctcccg 1300  
 gtgattgtga tgggtgttcc aggtgtgggt gggcgatgct gctacttgac 1350

cccaagctcc agtgtggaaa cttocttctt ggctgggttt ccagaactac 1400  
 agaggaatgg accacagtct tccaggggtcc ctctcgtcc accaaccggg 1450  
 agcctccacc ttggccatcc gtcagctatg aatgggtttt taaacaaacc 1500  
 cacgtcccag cctgggtaac atggtaaagc cccgtctcta caaaaaaatc 1550  
 caagttagcc gggcatgggtg gtgcgcacct gtagtcccag ctgcagtggg 1600  
 actgaggtgg aggtggaggt ggggggtggg agctgaggaa ggaggatcgc 1650  
 ttgagcctgg gaagtcgagg ctgcagtgag ctgagattgc accactgcac 1700  
 tccagcctgg gtgacagagc aagaccctgt ctcaaaaa 1738

<210> 361  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 361  
 Met Ser Cys Val Leu Gly Gly Val Ile Pro Leu Gly Leu Leu Phe  
 1 5 10 15  
 Leu Val Cys Gly Ser Gln Gly Tyr Leu Leu Pro Asn Val Thr Leu  
 20 25 30  
 Leu Glu Glu Leu Leu Ser Lys Tyr Gln His Asn Glu Ser His Ser  
 35 40 45  
 Arg Val Arg Arg Ala Ile Pro Arg Glu Asp Lys Glu Glu Ile Leu  
 50 55 60  
 Met Leu His Asn Lys Leu Arg Gly Gln Val Gln Pro Gln Ala Ser  
 65 70 75  
 Asn Met Glu Tyr Met Val Ser Ala Gly Ser Gly Arg Arg Gly Trp  
 80 85 90  
 His Arg Gly Trp Gly Leu Gly His Gln Pro Ala Leu Phe Pro Ser  
 95 100 105  
 Gln Leu Cys Ser Pro Ala Ser Ala Cys Asp Gly Trp Leu Arg Val  
 110 115 120  
 Ser Ser Gly Arg Gly Gly Ser Arg Leu Cys Ser Val Leu Phe Val  
 125 130 135  
 Cys Phe Glu Thr Gly Ser His Ser Ala Thr Asp Ala Gly Val Gln  
 140 145 150  
 Trp His Asn Arg His Ala Leu Lys Pro  
 155

<210> 362  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<400> 362  
 aaggagaggc caccgggact tcagtgtctc ctccatcca ggagcgcagt 50

ggccactatg gggctctgggc tgcccccttgt cctcctcttg accctccttg 100  
gcagctcaca tggaacaggg cggggtatga ctttgcaact gaagctgaag 150  
gagtcttttc tgacaaatc ctcctatgag tccagcttcc tggaattgct 200  
tgaaaagctc tgocctctcc tccatctccc ttcagggacc agcgtcaccc 250  
tccaccatgc aagatctcaa caccatgttg tctgcaacac atgacagcca 300  
ttgaagcctg tgtccttctt ggcccgggct tttgggcccgg ggatgcagga 350  
ggcaggcccc gaccctgtct ttcagcaggc ccccacctc ctgagtggca 400  
ataaataaaa ttcggtatgc tg 422

<210> 363  
<211> 78  
<212> PRT  
<213> Homo sapiens

<400> 363  
Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly  
1 5 10 15  
Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu  
20 25 30  
Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu  
35 40 45  
Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly  
50 55 60  
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val  
65 70 75

Cys Asn Thr

<210> 364  
<211> 826  
<212> DNA  
<213> Homo sapiens

<400> 364  
aattgtatct gtgtaatgtt aaaacaaacg aaataaaata gaaggaaaaa 50  
ctttctgagt ttcaaaaaca acagactagt actctaaaga actcttttaa 100  
acaattaact gttaggattg cagttatgat tggatattat ttaattctgt 150  
ttctgatgtg gggttcctcc actgtgttct gtgtgctatt aatatttacc 200  
attgcagaag cttcattcag tgttgaaaat gaatgcttag tggatctgtg 250  
cctcttacgc atatgttaca aattatctgg agttcctaata caatgcagag 300  
ttccccctccc ctccgattgt tctaaataat tgaaagatgt ctgctgtgga 350  
aaaaggcatg tatttaaatac tgtatgattc tcaaccatct ttagttggga 400  
aaggctccttg aaagccaatg gaaatacttt ttttttttct tggcactaat 450

caagtgagtg ttaccttttc acttagtagg atgtgttggtt acgctagtaa 500  
aatagaaacc tgtgtttatt ctgaggtatt ttagaaacaa cagccatcat 550  
tttattttat gtgtgtgttc ttggctgtat tcataaatta tatattttgg 600  
gctatcaaat attacttcat tcaatataaa taacaatagt agaagttggtt 650  
tacttagata tgctttctag ttgcattttc tcagcctatg taagactact 700  
ttgttgtaat agcctttgaa atttacagta ctgtctctct actatcttca 750  
gattacttga ttcaaataaa ccaattatgt ttgtaattga tattaataaa 800  
accagaataa aagttcatat ctaccc 826

<210> 365  
<211> 67  
<212> PRT  
<213> Homo sapiens

<400> 365  
Met Ile Gly Tyr Tyr Leu Ile Leu Phe Leu Met Trp Gly Ser Ser  
1 5 10 15  
Thr Val Phe Cys Val Leu Leu Ile Phe Thr Ile Ala Glu Ala Ser  
20 25 30  
Phe Ser Val Glu Asn Glu Cys Leu Val Asp Leu Cys Leu Leu Arg  
35 40 45  
Ile Cys Tyr Lys Leu Ser Gly Val Pro Asn Gln Cys Arg Val Pro  
50 55 60  
Leu Pro Ser Asp Cys Ser Lys  
65

<210> 366  
<211> 2475  
<212> DNA  
<213> Homo sapiens

<400> 366  
gaggatttgc cacagcagcg gatagagcag gagagcacca ccggagccct 50  
tgagacatcc ttgagaagag ccacagcata agagactgcc ctgcttggtg 100  
ttttgcagga tgatggtggc ccttcgagga gcttctgcat tgctggttct 150  
gttccttgca gcttttctgc ccccgccgca gtgtaccag gaccagcca 200  
tggtgcatta catctaccag cgctttcgag tcttgagca agggctggaa 250  
aatgtaccc aagcaacgag ggcatacatt caagaattcc aagagttctc 300  
aaaaaatata tctgtcatgc tgggaagatg tcagacctac acaagtgagt 350  
acaagagtgc agtgggtaac ttggcactga gagttgaacg tgcccaacgg 400  
gagattgact acatacaata ccttcgagag gctgacgagt gcatcgtatc 450  
agaggacaag aactggcag aaatgttgct ccaagaagct gaagaagaga 500

aaaagatccg gactctgctg aatgcaagct gtgacaacat gctgatgggc 550  
 ataaagtctt tgaaaatagt gaagaagatg atggacacac atggctcttg 600  
 gatgaaagat gctgtotata actctccaaa ggtgtactta ttaattggat 650  
 ccagaaacaa cactgttttg gaatttgcaa acatacgggc attcatggag 700  
 gataacacca agccagctcc ccggaagcaa atcctaacac tttcctggca 750  
 gggaacaggc caagtgatct acaaagggtt tctatttttt cataaccaag 800  
 caacttctaa tgagataatc aaatataacc tgcagaagag gactgtggaa 850  
 gatcgaatgc tgctcccagg aggggtaggc cgagcattgg tttaccagca 900  
 ctccccctca acttacattg acctggctgt ggatgagcat gggctctggg 950  
 ccatccactc tgggccaggc acccatagcc atttggttct cacaaagatt 1000  
 gagccgggca cactgggagt ggagcattca tgggataccc catgcagaag 1050  
 ccaggatgct gaagcctcat tctctttgtg tggggttctc tatgtggtct 1100  
 acagtactgg gggccagggc cctcatcgca tcacctgcat ctatgatcca 1150  
 ctgggcacta tcagtgagga ggacttgccc aacttgttct tccccaagag 1200  
 accaagaagt cactccatga tccattacaa cccagagat aagcagctct 1250  
 atgcctggaa tgaaggaaac cagatcattt acaaactcca gacaaagaga 1300  
 aagctgcctc tgaagtaatg cattacagct gtgagaaaga gcaactgtggc 1350  
 tttggcagct gttctacagg acagtgaggc tatagcccct tcacaatata 1400  
 gtatccctct aatcacacac aggaagagtg tgtagaagtg gaaatacgta 1450  
 tgccctcttt cccaaatgtc actgccttag gtatcttcca agagcttaga 1500  
 tgagagcata tcatcaggaa agtttcaaca atgtccatta ctccccaaa 1550  
 cctcctggct ctcaaggatg accacattct gatacagcct acttcaagcc 1600  
 ttttgtttta ctgctcccca gcatttactg taactctgcc atcttccctc 1650  
 ccacaattag agttgtatgc cagcccctaa tattcaccac tggcttttct 1700  
 ctcccctggc ctttgctgaa gctcttcct ctttttcaa tgtctattga 1750  
 tattctccca ttttactgc ccaactaaaa tactattaat atttctttct 1800  
 tttcttttct ttttttgag acaaggctc actatgttgc ccaggctgg 1850  
 ctcaaactcc agagctcaag agatcctcct gcctcagcct cctaagtacc 1900  
 tgggattaca ggcattgtgc accacacctg gcttaaaata ctatttctta 1950  
 ttgaggttta acctctattt cccctagccc tgccttcca ctaagcttgg 2000  
 tagatgtaat aataaagtga aaatattaac atttgaatat cgctttccag 2050  
 gtgtggagtg tttgcacatc attgaattct cgtttcacct ttgtgaaaca 2100

tgcacaagtc ttacagctg tcattctaga gtttaggtga gtaacacaat 2150  
 tacaagtgga aagatacagc tagaaaatac tacaatccc atagtttttc 2200  
 cattgcccaa ggaagcatca aatacgatg tttgttcacc tactcttata 2250  
 gtcaatgcgt tcatcgtttc agcctaaaaa taatagtctg tcccttttagc 2300  
 cagttttcat gtctgcacaa gacctttcaa taggcctttc aaatgataat 2350  
 tcctccagaa aaccagtcta agggtagagga ccccaactct agcctcctct 2400  
 tgtcttgctg tcctctgttt ctctctttct gctttaaatt caataaaagt 2450  
 gacactgagc aaaaaaaaaa aaaaa 2475

<210> 367  
 <211> 402  
 <212> PRT  
 <213> Homo sapiens

<400> 367  
 Met Met Val Ala Leu Arg Gly Ala Ser Ala Leu Leu Val Leu Phe  
 1 5 10 15  
 Leu Ala Ala Phe Leu Pro Pro Pro Gln Cys Thr Gln Asp Pro Ala  
 20 25 30  
 Met Val His Tyr Ile Tyr Gln Arg Phe Arg Val Leu Glu Gln Gly  
 35 40 45  
 Leu Glu Lys Cys Thr Gln Ala Thr Arg Ala Tyr Ile Gln Glu Phe  
 50 55 60  
 Gln Glu Phe Ser Lys Asn Ile Ser Val Met Leu Gly Arg Cys Gln  
 65 70 75  
 Thr Tyr Thr Ser Glu Tyr Lys Ser Ala Val Gly Asn Leu Ala Leu  
 80 85 90  
 Arg Val Glu Arg Ala Gln Arg Glu Ile Asp Tyr Ile Gln Tyr Leu  
 95 100 105  
 Arg Glu Ala Asp Glu Cys Ile Val Ser Glu Asp Lys Thr Leu Ala  
 110 115 120  
 Glu Met Leu Leu Gln Glu Ala Glu Glu Glu Lys Lys Ile Arg Thr  
 125 130 135  
 Leu Leu Asn Ala Ser Cys Asp Asn Met Leu Met Gly Ile Lys Ser  
 140 145 150  
 Leu Lys Ile Val Lys Lys Met Met Asp Thr His Gly Ser Trp Met  
 155 160 165  
 Lys Asp Ala Val Tyr Asn Ser Pro Lys Val Tyr Leu Leu Ile Gly  
 170 175 180  
 Ser Arg Asn Asn Thr Val Trp Glu Phe Ala Asn Ile Arg Ala Phe  
 185 190 195  
 Met Glu Asp Asn Thr Lys Pro Ala Pro Arg Lys Gln Ile Leu Thr  
 200 205 210

Leu	Ser	Trp	Gln	Gly	Thr	Gly	Gln	Val	Ile	Tyr	Lys	Gly	Phe	Leu	215	220	225
Phe	Phe	His	Asn	Gln	Ala	Thr	Ser	Asn	Glu	Ile	Ile	Lys	Tyr	Asn	230	235	240
Leu	Gln	Lys	Arg	Thr	Val	Glu	Asp	Arg	Met	Leu	Leu	Pro	Gly	Gly	245	250	255
Val	Gly	Arg	Ala	Leu	Val	Tyr	Gln	His	Ser	Pro	Ser	Thr	Tyr	Ile	260	265	270
Asp	Leu	Ala	Val	Asp	Glu	His	Gly	Leu	Trp	Ala	Ile	His	Ser	Gly	275	280	285
Pro	Gly	Thr	His	Ser	His	Leu	Val	Leu	Thr	Lys	Ile	Glu	Pro	Gly	290	295	300
Thr	Leu	Gly	Val	Glu	His	Ser	Trp	Asp	Thr	Pro	Cys	Arg	Ser	Gln	305	310	315
Asp	Ala	Glu	Ala	Ser	Phe	Leu	Leu	Cys	Gly	Val	Leu	Tyr	Val	Val	320	325	330
Tyr	Ser	Thr	Gly	Gly	Gln	Gly	Pro	His	Arg	Ile	Thr	Cys	Ile	Tyr	335	340	345
Asp	Pro	Leu	Gly	Thr	Ile	Ser	Glu	Glu	Asp	Leu	Pro	Asn	Leu	Phe	350	355	360
Phe	Pro	Lys	Arg	Pro	Arg	Ser	His	Ser	Met	Ile	His	Tyr	Asn	Pro	365	370	375
Arg	Asp	Lys	Gln	Leu	Tyr	Ala	Trp	Asn	Glu	Gly	Asn	Gln	Ile	Ile	380	385	390
Tyr	Lys	Leu	Gln	Thr	Lys	Arg	Lys	Leu	Pro	Leu	Lys				395	400	

<210> 368  
 <211> 2281  
 <212> DNA  
 <213> Homo sapiens

<400> 368  
 gggcgccgc gtactcacta gctgaggtgg cagtgggtcc accaacaatgg 50  
 agctctcgca gatgtcggag ctcatggggc tgtcgggtgtt gcttgggctg 100  
 ctggccctga tggcgacggc ggcggtagcg cgggggtggc tgcgcgcggg 150  
 ggaggagagg agcggccggc ccgcctgccaaaagcaaat ggatttccac 200  
 ctgacaaatc ttcgggatcc aagaagcaga aacaatatca gcggattcgg 250  
 aaggagaagc ctcaacaaca caacttcacc caccgcctcc tggctgcagc 300  
 tctgaagagc cacagcggga acatatcttg catggacttt agcagcaatg 350  
 gcaaatacct ggctacctgt gcagatgata gcaccatccg catctggagc 400  
 accaaggact tctgcagcg agagcaccgc agcatgagag ccaacgtgga 450

gctggaccac gccaccctgg tgcgcttcag ccctgactgc agagccttca 500  
tcgtctggct ggccaacggg gacaccctcc gtgtcttcaa gatgaccaag 550  
cgggaggatg ggggctacac cttcacagcc accccagagg acttccctaa 600  
aaagcacaag gcgcctgtca tcgacattgg cattgctaac acagggaagt 650  
ttatcatgac tgcctccagt gacaccactg tcctcatctg gagcctgaag 700  
ggtcaagtgc tgtctacat caacaccaac cagatgaaca acacacacgc 750  
tgctgtatct ccctgtggca gatttgtagc ctctgtgtggc ttcaccccag 800  
atgtgaagggt ttgggaagtc tgctttggaa agaaggggga gttccaggag 850  
gtggtgcgag ccttcgaact aaagggccac tccgcggctg tgcactcgtt 900  
tgctttctcc aacgactcac ggaggatggc ttctgtctcc aaggatggta 950  
catggaaact gtgggacaca gatgtggaat acaagaagaa gcaggacccc 1000  
tacttgctga agacaggccg ctttgaagag gcggcgggtg ccgcgcctg 1050  
ccgcctggcc ctctccccc acgcccaggt cttggccttg gccagtggca 1100  
gtagtattca tctctacaat acccggcggg gcgagaagga ggagtgcctt 1150  
gagcgggtcc atggcgagt tctcgccaac ttgtcctttg acatcactgg 1200  
ccgctttctg gcctcctgtg gggaccgggc ggtgcggctg tttcacaaca 1250  
ctcctggcca ccgagccatg gtggaggaga tgcagggcca cctgaagcgg 1300  
gcctccaacg agagcacccg ccagaggctg cagcagcagc tgacccaggc 1350  
ccaagagacc ctgaagagcc tgggtgccct gaagaagtga ctctgggagg 1400  
gcccggcgca gaggattgag gaggaggat ctggcctcct catggcactg 1450  
ctgccatctt tcctcccagg tggaagcctt tcagaaggag tctcctgggt 1500  
ttcttactgg tggcctgct tcttcccatt gaaactactc ttgtctactt 1550  
aggtctctct cttcttgctg gctgtgactc ctccctgact agtggccaag 1600  
gtgcttttct tcctcccagg ccagtggtt ggaatctgtc cccacctggc 1650  
actgaggaga atggtagaga ggagaggaga gagagagaga atgtgatttt 1700  
tggccttgct gcagcacatc ctcacacca aagaagtttg taaatgttcc 1750  
agaacaacct agagaacacc tgagtactaa gcagcagttt tgcaaggatg 1800  
ggagactggg atagcttccc atcacagaac tgtgttccat caaaaagaca 1850  
ctaagggatt tccttctggg cctcagttct atttgtaaga tggagaataa 1900  
tcctctctgt gaactccttg caaagatgat atgaggctaa gagaatatca 1950  
agtccccagg tctggaagaa aagtagaaaa gagtagtact attgtccaat 2000  
gtcatgaaag tggtaaaagt gggaaaccagt gtgctttgaa accaaattag 2050

aaacacattc cttgggaagg caaagttttc tgggacttga tcatacatTT 2100  
 tatatggttg ggactttctc cttcgggaga tgatatcttg tttaaggaga 2150  
 cctcttttca gttcatcaag ttcacagat atttgagtgc ccactctgtg 2200  
 cccaaataaa tatgagctgg ggattaaaaa aaaaaaaaaa aaaaaaaaaa 2250  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2281

<210> 369  
 <211> 447  
 <212> PRT  
 <213> Homo sapiens

<400> 369  
 Met Glu Leu Ser Gln Met Ser Glu Leu Met Gly Leu Ser Val Leu  
 1 5 10 15  
 Leu Gly Leu Leu Ala Leu Met Ala Thr Ala Ala Val Ala Arg Gly  
 20 25 30  
 Trp Leu Arg Ala Gly Glu Glu Arg Ser Gly Arg Pro Ala Cys Gln  
 35 40 45  
 Lys Ala Asn Gly Phe Pro Pro Asp Lys Ser Ser Gly Ser Lys Lys  
 50 55 60  
 Gln Lys Gln Tyr Gln Arg Ile Arg Lys Glu Lys Pro Gln Gln His  
 65 70 75  
 Asn Phe Thr His Arg Leu Leu Ala Ala Ala Leu Lys Ser His Ser  
 80 85 90  
 Gly Asn Ile Ser Cys Met Asp Phe Ser Ser Asn Gly Lys Tyr Leu  
 95 100 105  
 Ala Thr Cys Ala Asp Asp Arg Thr Ile Arg Ile Trp Ser Thr Lys  
 110 115 120  
 Asp Phe Leu Gln Arg Glu His Arg Ser Met Arg Ala Asn Val Glu  
 125 130 135  
 Leu Asp His Ala Thr Leu Val Arg Phe Ser Pro Asp Cys Arg Ala  
 140 145 150  
 Phe Ile Val Trp Leu Ala Asn Gly Asp Thr Leu Arg Val Phe Lys  
 155 160 165  
 Met Thr Lys Arg Glu Asp Gly Gly Tyr Thr Phe Thr Ala Thr Pro  
 170 175 180  
 Glu Asp Phe Pro Lys Lys His Lys Ala Pro Val Ile Asp Ile Gly  
 185 190 195  
 Ile Ala Asn Thr Gly Lys Phe Ile Met Thr Ala Ser Ser Asp Thr  
 200 205 210  
 Thr Val Leu Ile Trp Ser Leu Lys Gly Gln Val Leu Ser Thr Ile  
 215 220 225  
 Asn Thr Asn Gln Met Asn Asn Thr His Ala Ala Val Ser Pro Cys  
 230 235 240

Gly	Arg	Phe	Val	Ala	Ser	Cys	Gly	Phe	Thr	Pro	Asp	Val	Lys	Val	
				245					250					255	
Trp	Glu	Val	Cys	Phe	Gly	Lys	Lys	Gly	Glu	Phe	Gln	Glu	Val	Val	
				260					265					270	
Arg	Ala	Phe	Glu	Leu	Lys	Gly	His	Ser	Ala	Ala	Val	His	Ser	Phe	
				275					280					285	
Ala	Phe	Ser	Asn	Asp	Ser	Arg	Arg	Met	Ala	Ser	Val	Ser	Lys	Asp	
				290					295					300	
Gly	Thr	Trp	Lys	Leu	Trp	Asp	Thr	Asp	Val	Glu	Tyr	Lys	Lys	Lys	
				305					310					315	
Gln	Asp	Pro	Tyr	Leu	Leu	Lys	Thr	Gly	Arg	Phe	Glu	Glu	Ala	Ala	
				320					325					330	
Gly	Ala	Ala	Pro	Cys	Arg	Leu	Ala	Leu	Ser	Pro	Asn	Ala	Gln	Val	
				335					340					345	
Leu	Ala	Leu	Ala	Ser	Gly	Ser	Ser	Ile	His	Leu	Tyr	Asn	Thr	Arg	
				350					355					360	
Arg	Gly	Glu	Lys	Glu	Glu	Cys	Phe	Glu	Arg	Val	His	Gly	Glu	Cys	
				365					370					375	
Ile	Ala	Asn	Leu	Ser	Phe	Asp	Ile	Thr	Gly	Arg	Phe	Leu	Ala	Ser	
				380					385					390	
Cys	Gly	Asp	Arg	Ala	Val	Arg	Leu	Phe	His	Asn	Thr	Pro	Gly	His	
				395					400					405	
Arg	Ala	Met	Val	Glu	Glu	Met	Gln	Gly	His	Leu	Lys	Arg	Ala	Ser	
				410					415					420	
Asn	Glu	Ser	Thr	Arg	Gln	Arg	Leu	Gln	Gln	Gln	Leu	Thr	Gln	Ala	
				425					430					435	
Gln	Glu	Thr	Leu	Lys	Ser	Leu	Gly	Ala	Leu	Lys	Lys				
				440					445						

<210> 370  
 <211> 1415  
 <212> DNA  
 <213> Homo sapiens

<400> 370  
 tggcctcccc agcttgccag gcacaaggct gagcgggagg aagcgagagg 50  
 catctaagca ggcagtgttt tgccttcacc ccaagtgacc atgagaggtg 100  
 ccacgcgagt ctcaatcatg ctctctctag taactgtgtc tgactgtgct 150  
 gtgatcacag gggcctgtga gcgggatgtc cagtgtgggg caggcacctg 200  
 ctgtgccatc agcotgtggc ttogaggggt gcggatgtgc accccgctgg 250  
 ggcggaagg cgaggagtgc caccocggca gccacaaggc ccccttcttc 300  
 aggaaacgca agcaccacac ctgtccttgc ttgcccaacc tgetgtgtc 350  
 caggttcccg gacggcaggt accgctgtgc catggacttg aagaacatca 400

atttttaggc gcttgcoctgg tctcaggata cccaccatcc ttttcctgag 450  
 cacagcctgg atttttatatt ctgccatgaa acccagctcc catgactctc 500  
 ccagtcccta cactgactac cctgatctct cttgtctagt acgcacatat 550  
 gcacacaggc agacatacct cccatcatga catggtcccc aggcctggcct 600  
 gaggatgtca cagcttgagg ctgtggtgtg aaagggtggc agcctgggtc 650  
 tcttcctgc tcaggctgcc agagaggtgg taaatggcag aaaggacatt 700  
 cccctcccc tcccagggtg acctgctctc tttcctgggc cctgcccctc 750  
 tccccacatg tatccctcgg tctgaattag acattcctgg gcacaggctc 800  
 ttgggtgcat tgctcagagt cccaggctct ggctgaccc tcaggccctt 850  
 cacgtgaggt ctgtgaggac caatttgtgg gtagttcatc ttccctcgat 900  
 tgggttaactc cttagtttca gaccacagac tcaagattgg ctcttcccag 950  
 agggcagcag acagtcaccc caaggcaggt gtagggagcc caggagggcc 1000  
 aatcagcccc ctgaagactc tgggtcccagt cagcctgtgg cttgtggcct 1050  
 gtgacctgtg accttctgcc agaattgtca tgcctctgag gccccctctt 1100  
 accacacttt accagttaac cactgaagcc cccaattccc acagcttttc 1150  
 cattaanaatg caaatggtgg tggttcaatc taatctgata ttgacatatt 1200  
 agaaggcaat taggggtgtt ccttaaaca ctcctttcca aggatcagcc 1250  
 ctgagagcag gttggtgact ttgaggagg cagtcctctg tccagattgg 1300  
 ggtgggagca agggacaggg agcagggcag gggctgaaag gggcactgat 1350  
 tcagaccagg gaggcaacta cacaccaaca tgctggcttt agaataaaag 1400  
 caccaactga aaaaa 1415

<210> 371  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 371  
 Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr  
 1 5 10 15  
 Val Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val  
 20 25 30  
 Gln Cys Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg  
 35 40 45  
 Gly Leu Arg Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys  
 50 55 60  
 His Pro Gly Ser His Lys Val Pro Phe Phe Arg Lys Arg Lys His  
 65 70 75

His	Thr	Cys	Pro	Cys	Leu	Pro	Asn	Leu	Leu	Cys	Ser	Arg	Phe	Pro
				80					85					90
Asp	Gly	Arg	Tyr	Arg	Cys	Ser	Met	Asp	Leu	Lys	Asn	Ile	Asn	Phe
				95					100					105

<210> 372  
 <211> 1281  
 <212> DNA  
 <213> Homo sapiens

<400> 372  
 agcgcccggg cgtcggggcg gtaaaaggcc ggcagaaggg aggcacttga 50  
 gaaatgtctt tcctccagga cccaagtctt ttcaccatgg ggatgtgggc 100  
 cattggtgca ggagccctgg gggctgctgc cttggcattg ctgcttgcca 150  
 acacagacgt gtttctgtcc aagcccaga aagcggccct ggagtacctg 200  
 gaggatatag acctgaaaac actggagaag gaaccaagga ctttcaaagc 250  
 aaaggagcta tgggaaaaaa atggagctgt gattatggcc gtgcggaggc 300  
 caggctgttt cctctgtcga gaggaagctg cggatctgtc ctccctgaaa 350  
 agcatgttgg accagctggg cgtcccctc tatgcagtgg taaaggagca 400  
 catcaggact gaagtgaagg atttcagcc ttatttcaaa ggagaaatct 450  
 tcctggatga aaagaaaaag ttctatgggc cacaaggcg gaagatgatg 500  
 tttatgggat ttatccgtct gggagtgtgg tacaacttot tccgagcctg 550  
 gaacggaggc ttctctggaa acctggaagg agaaggcttc atccttgggg 600  
 gagttttcgt ggtgggatca ggaaagcagg gcattcttot tgagcacoga 650  
 gaaaaagaat ttggagacaa agtaaaccta ctttctgttc tggaagctgc 700  
 taagatgatc aaaccacaga ctttggcctc agagaaaaaa tgattgtgtg 750  
 aaactgcca gctcagggat aaccaggac attcacctgt gttcatggga 800  
 tgtattgttt ccaactgtgt cctaaggag tgagaaacc atttatactc 850  
 tactctcagt atggattatt aatgtatttt aatattctgt ttagggccac 900  
 taaggcaaaa tagcccaaaa acaagactga caaaaatctg aaaaactaat 950  
 gaggattatt aagctaaaac ctgggaaata ggaggcttaa aattgactgc 1000  
 caggctgggt gcagtggctc acacctgtaa tcccagcact ttgggaggcc 1050  
 aaggtgagca agtcacttga ggtcgggagt tcgagaccag cctgagcaac 1100  
 atggcgaaac cccgtctcta ctaaaaatac aaaaatcacc cgggtgtggt 1150  
 ggcaggcacc tgtagtccca gctaccggg aggctgaggc aggagaatca 1200  
 cttgaacctg ggaggtggag gttgcggtga gctgagatca caccactgta 1250  
 ttccagcctg ggtgactgag actctaaacta a 1281

<210> 373  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 373  
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp  
 1 5 10 15  
 Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu  
 20 25 30  
 Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala  
 35 40 45  
 Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu  
 50 55 60  
 Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala  
 65 70 75  
 Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu  
 80 85 90  
 Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu  
 95 100 105  
 Gly Val Pro Leu Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu  
 110 115 120  
 Val Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp  
 125 130 135  
 Glu Lys Lys Lys Phe Tyr Gly Pro Gln Arg Arg Lys Met Met Phe  
 140 145 150  
 Met Gly Phe Ile Arg Leu Gly Val Trp Tyr Asn Phe Phe Arg Ala  
 155 160 165  
 Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly Glu Gly Phe Ile  
 170 175 180  
 Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln Gly Ile Leu  
 185 190 195  
 Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn Leu Leu  
 200 205 210  
 Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu Ala  
 215 220 225  
 Ser Glu Lys Lys

<210> 374  
 <211> 744  
 <212> DNA  
 <213> Homo sapiens

<400> 374  
 acggaccgag ggttcgaggg agggacacgg accaggaacc tgagctaggt 50  
 caaagacgcc cgggccaggt gccccgtcgc aggtgcccot ggccggagat 100

gcggtaggag gggcgagcgc gagaagcccc ttcctcggcg ctgccaaacc 150  
 gccaccagc ccatggcgaa ccccgggctg gggctgcttc tggcgctggg 200  
 cctgccgttc ctgctggccc gctggggccg agcctggggg caaatacaga 250  
 ccactttctgc aaatgagaat agcactgttt tgccttcata caccagctcc 300  
 agctccgatg gcaacctgcg tccggaagcc atcactgcta tcatcgtggg 350  
 cttctccctc ttggctgcct tgctcctggc tgtggggctg gcactgttgg 400  
 tgcggaagct tcgggagaag cggcagacgg agggcaccta ccggcccagt 450  
 agcgaggagc agttctccca tgcagccgag gcccgggccc ctcaggactc 500  
 caaggagacg gtgcagggct gcctgcccat ctaggtcccc tctcctgcat 550  
 ctgtctccct tcattgctgt gtgaccttgg ggaaaggcag tgccctctct 600  
 gggcagtcag atccaccag tgcttaatag cagggaagaa ggtacttcaa 650  
 agactctgcc cctgaggtca agagaggatg gggctattca cttttatata 700  
 tttatataaa attagtagtg agatgtaaaa aaaaaaaaaa aaaa 744

<210> 375  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 375  
 Met Ala Asn Pro Gly Leu Gly Leu Leu Leu Ala Leu Gly Leu Pro  
 1 5 10 15  
 Phe Leu Leu Ala Arg Trp Gly Arg Ala Trp Gly Gln Ile Gln Thr  
 20 25 30  
 Thr Ser Ala Asn Glu Asn Ser Thr Val Leu Pro Ser Ser Thr Ser  
 35 40 45  
 Ser Ser Ser Asp Gly Asn Leu Arg Pro Glu Ala Ile Thr Ala Ile  
 50 55 60  
 Ile Val Val Phe Ser Leu Leu Ala Ala Leu Leu Leu Ala Val Gly  
 65 70 75  
 Leu Ala Leu Leu Val Arg Lys Leu Arg Glu Lys Arg Gln Thr Glu  
 80 85 90  
 Gly Thr Tyr Arg Pro Ser Ser Glu Glu Gln Phe Ser His Ala Ala  
 95 100 105  
 Glu Ala Arg Ala Pro Gln Asp Ser Lys Glu Thr Val Gln Gly Cys  
 110 115 120  
 Leu Pro Ile

<210> 376  
 <211> 713  
 <212> DNA  
 <213> Homo sapiens

<400> 376  
aatatatcat ctatttatca ttaatcaata atgtattcctt ttattccaat 50  
aacatttggg ttttgggatt ttaattttca aacacagcag aatgacattt 100  
tttctgtcac tattattatt gttggtatgt gaagctattt ggagatccaa 150  
ttcaggaagc aacacattgg agaatggcta ctttctatca agaaataaag 200  
agaaccacag tcaaccacac caatcatcctt tagaagacag tgtgactcct 250  
accaaagctg tcaaaaccac aggcaagggc atagttaaag gacggaatct 300  
tgactcaaga ggggttaattc ttggtgctga agcctggggc aggggtgtaa 350  
agaaaaacac ttagattcaa tgattgtaaa ttttaaggcaa atacacatat 400  
tagtattacc ttagtgtaat gtatccctgt catatataca ataaggtgaa 450  
attataagta ccctatgcag ttggctggac agttctaaat tggactttat 500  
taatttttaa aatcagtaac tgatttatca ctggctatgt gcttagatct 550  
acaggagatc atataatttg atacaaataa aagaaaagtg ttctctcccc 600  
ttacagaatt gacattttta atgcgataca gttagaatag gaaatatgac 650  
attagaaagg aagaatgaca gggagaaagg aaagaaggga aaatgttgcc 700  
aaggaaaaaa aaa 713

<210> 377  
<211> 90  
<212> PRT  
<213> Homo sapiens

<400> 377  
Met Thr Phe Phe Leu Ser Leu Leu Leu Leu Val Cys Glu Ala  
1 5 10 15  
Ile Trp Arg Ser Asn Ser Gly Ser Asn Thr Leu Glu Asn Gly Tyr  
20 25 30  
Phe Leu Ser Arg Asn Lys Glu Asn His Ser Gln Pro Thr Gln Ser  
35 40 45  
Ser Leu Glu Asp Ser Val Thr Pro Thr Lys Ala Val Lys Thr Thr  
50 55 60  
Gly Lys Gly Ile Val Lys Gly Arg Asn Leu Asp Ser Arg Gly Leu  
65 70 75  
Ile Leu Gly Ala Glu Ala Trp Gly Arg Gly Val Lys Lys Asn Thr  
80 85 90

<210> 378  
<211> 3265  
<212> DNA  
<213> Homo sapiens

<400> 378  
gccaggaata actagagagg aacaatgggg ttattcagag gttttgtttt 50

cctcttagtt ctgtgctgc tgcaccagtc aaatacttcc ttcattaagc 100  
tgaataataa tggctttgaa gatattgtca ttgttataga tcttagtgtg 150  
ccagaagatg aaaaaataat tgaacaaata gaggatatgg tgactacagc 200  
ttctacgtac ctgtttgaag ccacagaaaa aagatTTTTT ttcaaaaatg 250  
tatctatatt aattcctgag aattggaagg aaaatcctca gtacaaaagg 300  
ccaaaacatg aaaaccataa acatgctgat gttatagttg caccacctac 350  
actcccaggt agagatgaac catacaccaa gcagttcaca gaatgtggag 400  
agaaaggcga atacattcac ttcacccctg accttctact tggaaaaaaa 450  
caaaatgaat atggaccacc aggcaaactg tttgtccatg agtgggctca 500  
cctccggtgg ggagtgtttg atgagtacaa tgaagatcag cctttctacc 550  
gtgctaagtc aaaaaaatc gaagcaacaa ggtgttccgc aggtatctct 600  
ggtagaaata gagtttataa gtgtcaagga ggcagctgtc ttagtagagc 650  
atgcagaatt gattctacaa caaaactgta tggaaaagat tgtcaattct 700  
ttcctgataa agtacaaaca gaaaagcat ccataatgtt tatgcaaagt 750  
attgattctg ttgttgaatt ttgtaacgaa aaaaccata atcaagaagc 800  
tccaagccta caaaacataa agtgcaattt tagaagtaca tgggaggtga 850  
ttagcaattc tgaggatttt aaaaacacca taccatggg gacaccacct 900  
cctccacctg tcttctcatt gctgaagatc agtcaaagaa ttgtgtgctt 950  
agttcttgat aagtctggaa gcatgggggg taaggaccgc ctaaatacgaa 1000  
tgaatcaagc agcaaaacat ttctgctgc agactgttga aaatggatcc 1050  
tgggtgggga tgggttcaatt tgatagtact gccactattg taaataagct 1100  
aatccaaata aaaagcagtg atgaaagaaa cacactcatg gcaggattac 1150  
ctacatatcc tctgggagga acttccatct gctctggaat taaatatgca 1200  
tttcaggtga ttggagagct acattcccaa ctcgatggat ccgaagtact 1250  
gctgctgact gatggggagg ataacactgc aagttcttgt attgatgaag 1300  
tgaaacaaag tggggccatt gttcatttta ttgctttggg aagagctgct 1350  
gatgaagcag taatagagat gagcaagata acaggaggaa gtcattttta 1400  
tgtttcagat gaagctcaga acaatggcct cattgatgct tttggggctc 1450  
ttacatcagg aaatactgat ctctcccaga agtcccttca gctcgaaagt 1500  
aagggattaa cactgaatag taatgcctgg atgaacgaca ctgtcataat 1550  
tgatagtaca gtgggaaagg acacgttctt tctcatcaca tggaacagtc 1600  
tgctcccag tatttctctc tgggatccca gtggaacaat aatggaaaa 1650

ttcacagtgg atgcaacttc caaaatggcc tatctcagta ttccaggaac 1700  
 tgcaaagggtg ggcacttggg catacaatct tcaagccaaa gcgaacccag 1750  
 aaacattaac tattacagta acttctcgag cagcaaattc ttctgtgcct 1800  
 ccaatcacag tgaatgctaa aatgaataag gacgtaaaca gtttccccag 1850  
 cccaatgatt gtttacgcag aaattctaca aggatatgta cctgttcttg 1900  
 gagccaatgt gactgctttc attgaatcac agaatggaca tacagaagtt 1950  
 ttggaacttt tggataatgg tgcaggcgct gattctttca agaatgatgg 2000  
 agtctactcc aggtatttta cagcatatac agaaaatggc agatatagct 2050  
 taaaagtctg ggctcatgga ggagcaaaaca ctgccaggct aaaattacgg 2100  
 cctccactga atagagccgc gtacatacca ggctgggtag tgaacgggga 2150  
 aattgaagca aaccgcgcaa gacctgaaat tgatgaggat actcagacca 2200  
 ccttgaggga tticagccga acagcatccg gaggtgcatt tgtggatatca 2250  
 caagtcccaa gccttcctct gcctgaccaa taccaccaa gtcaaatcac 2300  
 agaccttgat gccacagttc atgaggataa gattattctt acatggacag 2350  
 caccaggaga taattttgat gttggaaaag ttcaacgtta tatcataaga 2400  
 ataagtgcaa gtattcttga tctaagagac agttttgatg atgctcttca 2450  
 agtaaatact actgatctgt caccaaagga ggccaactcc aaggaaagct 2500  
 ttgcatttaa accagaaaat atctcagaag aaaatgcaac ccacataatt 2550  
 attgccatta aaagtataga taaaagcaat ttgacatcaa aagtatccaa 2600  
 cattgcacaa gtaactttgt ttatccctca agcaaatcct gatgacattg 2650  
 atcctacacc tactcctact cctactccta ctctgataa aagtcataat 2700  
 totggagtta atatttctac gctgggtattg tctgtgattg ggtctgttgt 2750  
 aattgttaac tttattttta gtaccaccat ttgaacctta acgaagaaaa 2800  
 aaatcttcaa gtagacctag aagagagttt taaaaaaca aacaatgtaa 2850  
 gttaaaggata tttctgaatc ttaaaattca tcccatgtgt gatcataaac 2900  
 tcataaaaaat aatttttaaga tgtcggaaaa ggatactttg attaaataaa 2950  
 aacactcatg gatatgtaaa aactgtcaag attaaaattt aatagtttca 3000  
 tttatttggt attttatttg taagaaatag tgatgaacaa agatcctttt 3050  
 tcatactgat acctggttgt atattatttg atgcaacagt tttctgaaat 3100  
 gatattttcaa attgcatcaa gaaattaaaa tcatctatct gagtagtcaa 3150  
 aatacaagta aaggagagca aataaacaac atttgaaaaa aaaaaaaaaa 3200  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3250

aaaaaaaaaa aaaaa 3265

<210> 379

<211> 919

<212> PRT

<213> Homo sapiens

<400> 379

Met	Gly	Leu	Phe	Arg	Gly	Phe	Val	Phe	Leu	Leu	Val	Leu	Cys	Leu	
1				5					10					15	
Leu	His	Gln	Ser	Asn	Thr	Ser	Phe	Ile	Lys	Leu	Asn	Asn	Asn	Gly	
				20					25					30	
Phe	Glu	Asp	Ile	Val	Ile	Val	Ile	Asp	Pro	Ser	Val	Pro	Glu	Asp	
				35					40					45	
Glu	Lys	Ile	Ile	Glu	Gln	Ile	Glu	Asp	Met	Val	Thr	Thr	Ala	Ser	
				50					55					60	
Thr	Tyr	Leu	Phe	Glu	Ala	Thr	Glu	Lys	Arg	Phe	Phe	Phe	Lys	Asn	
				65					70					75	
Val	Ser	Ile	Leu	Ile	Pro	Glu	Asn	Trp	Lys	Glu	Asn	Pro	Gln	Tyr	
				80					85					90	
Lys	Arg	Pro	Lys	His	Glu	Asn	His	Lys	His	Ala	Asp	Val	Ile	Val	
				95					100					105	
Ala	Pro	Pro	Thr	Leu	Pro	Gly	Arg	Asp	Glu	Pro	Tyr	Thr	Lys	Gln	
				110					115					120	
Phe	Thr	Glu	Cys	Gly	Glu	Lys	Gly	Glu	Tyr	Ile	His	Phe	Thr	Pro	
				125					130					135	
Asp	Leu	Leu	Leu	Gly	Lys	Lys	Gln	Asn	Glu	Tyr	Gly	Pro	Pro	Gly	
				140					145					150	
Lys	Leu	Phe	Val	His	Glu	Trp	Ala	His	Leu	Arg	Trp	Gly	Val	Phe	
				155					160					165	
Asp	Glu	Tyr	Asn	Glu	Asp	Gln	Pro	Phe	Tyr	Arg	Ala	Lys	Ser	Lys	
				170					175					180	
Lys	Ile	Glu	Ala	Thr	Arg	Cys	Ser	Ala	Gly	Ile	Ser	Gly	Arg	Asn	
				185					190					195	
Arg	Val	Tyr	Lys	Cys	Gln	Gly	Gly	Ser	Cys	Leu	Ser	Arg	Ala	Cys	
				200					205					210	
Arg	Ile	Asp	Ser	Thr	Thr	Lys	Leu	Tyr	Gly	Lys	Asp	Cys	Gln	Phe	
				215					220					225	
Phe	Pro	Asp	Lys	Val	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Met	
				230					235					240	
Gln	Ser	Ile	Asp	Ser	Val	Val	Glu	Phe	Cys	Asn	Glu	Lys	Thr	His	
				245					250					255	
Asn	Gln	Glu	Ala	Pro	Ser	Leu	Gln	Asn	Ile	Lys	Cys	Asn	Phe	Arg	
				260					265					270	
Ser	Thr	Trp	Glu	Val	Ile	Ser	Asn	Ser	Glu	Asp	Phe	Lys	Asn	Thr	

275										280					285				
Ile	Pro	Met	Val	Thr	Pro	Pro	Pro	Pro	Pro	Val	Phe	Ser	Leu	Leu					
				290										300					
Lys	Ile	Ser	Gln	Arg	Ile	Val	Cys	Leu	Val	Leu	Asp	Lys	Ser	Gly					
				305					310					315					
Ser	Met	Gly	Gly	Lys	Asp	Arg	Leu	Asn	Arg	Met	Asn	Gln	Ala	Ala					
				320					325					330					
Lys	His	Phe	Leu	Leu	Gln	Thr	Val	Glu	Asn	Gly	Ser	Trp	Val	Gly					
				335					340					345					
Met	Val	His	Phe	Asp	Ser	Thr	Ala	Thr	Ile	Val	Asn	Lys	Leu	Ile					
				350					355					360					
Gln	Ile	Lys	Ser	Ser	Asp	Glu	Arg	Asn	Thr	Leu	Met	Ala	Gly	Leu					
				365					370					375					
Pro	Thr	Tyr	Pro	Leu	Gly	Gly	Thr	Ser	Ile	Cys	Ser	Gly	Ile	Lys					
				380					385					390					
Tyr	Ala	Phe	Gln	Val	Ile	Gly	Glu	Leu	His	Ser	Gln	Leu	Asp	Gly					
				395					400					405					
Ser	Glu	Val	Leu	Leu	Leu	Thr	Asp	Gly	Glu	Asp	Asn	Thr	Ala	Ser					
				410					415					420					
Ser	Cys	Ile	Asp	Glu	Val	Lys	Gln	Ser	Gly	Ala	Ile	Val	His	Phe					
				425					430					435					
Ile	Ala	Leu	Gly	Arg	Ala	Ala	Asp	Glu	Ala	Val	Ile	Glu	Met	Ser					
				440					445					450					
Lys	Ile	Thr	Gly	Gly	Ser	His	Phe	Tyr	Val	Ser	Asp	Glu	Ala	Gln					
				455					460					465					
Asn	Asn	Gly	Leu	Ile	Asp	Ala	Phe	Gly	Ala	Leu	Thr	Ser	Gly	Asn					
				470					475					480					
Thr	Asp	Leu	Ser	Gln	Lys	Ser	Leu	Gln	Leu	Glu	Ser	Lys	Gly	Leu					
				485					490					495					
Thr	Leu	Asn	Ser	Asn	Ala	Trp	Met	Asn	Asp	Thr	Val	Ile	Ile	Asp					
				500					505					510					
Ser	Thr	Val	Gly	Lys	Asp	Thr	Phe	Phe	Leu	Ile	Thr	Trp	Asn	Ser					
				515					520					525					
Leu	Pro	Pro	Ser	Ile	Ser	Leu	Trp	Asp	Pro	Ser	Gly	Thr	Ile	Met					
				530					535					540					
Glu	Asn	Phe	Thr	Val	Asp	Ala	Thr	Ser	Lys	Met	Ala	Tyr	Leu	Ser					
				545					550					555					
Ile	Pro	Gly	Thr	Ala	Lys	Val	Gly	Thr	Trp	Ala	Tyr	Asn	Leu	Gln					
				560					565					570					
Ala	Lys	Ala	Asn	Pro	Glu	Thr	Leu	Thr	Ile	Thr	Val	Thr	Ser	Arg					
				575					580					585					
Ala	Ala	Asn	Ser	Ser	Val	Pro	Pro	Ile	Thr	Val	Asn	Ala	Lys	Met					

590					595					600				
Asn	Lys	Asp	Val	Asn	Ser	Phe	Pro	Ser	Pro	Met	Ile	Val	Tyr	Ala
				605										615
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				620										630
Ala	Phe	Ile	Glu	Ser	Gln	Asn	Gly	His	Thr	Glu	Val	Leu	Glu	Leu
				635										645
Leu	Asp	Asn	Gly	Ala	Gly	Ala	Asp	Ser	Phe	Lys	Asn	Asp	Gly	Val
				650										660
Tyr	Ser	Arg	Tyr	Phe	Thr	Ala	Tyr	Thr	Glu	Asn	Gly	Arg	Tyr	Ser
				665										675
Leu	Lys	Val	Arg	Ala	His	Gly	Gly	Ala	Asn	Thr	Ala	Arg	Leu	Lys
				680										690
Leu	Arg	Pro	Pro	Leu	Asn	Arg	Ala	Ala	Tyr	Ile	Pro	Gly	Trp	Val
				695										705
Val	Asn	Gly	Glu	Ile	Glu	Ala	Asn	Pro	Pro	Arg	Pro	Glu	Ile	Asp
				710										720
Glu	Asp	Thr	Gln	Thr	Thr	Leu	Glu	Asp	Phe	Ser	Arg	Thr	Ala	Ser
				725										735
Gly	Gly	Ala	Phe	Val	Val	Ser	Gln	Val	Pro	Ser	Leu	Pro	Leu	Pro
				740										750
Asp	Gln	Tyr	Pro	Pro	Ser	Gln	Ile	Thr	Asp	Leu	Asp	Ala	Thr	Val
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His	Glu	Asp	Lys	Ile	Ile	Leu	Thr	Trp	Thr	Ala	Pro	Gly	Asp	Asn
				770										780
Phe	Asp	Val	Gly	Lys	Val	Gln	Arg	Tyr	Ile	Ile	Arg	Ile	Ser	Ala
				785										795
Ser	Ile	Leu	Asp	Leu	Arg	Asp	Ser	Phe	Asp	Asp	Ala	Leu	Gln	Val
				800										810
Asn	Thr	Thr	Asp	Leu	Ser	Pro	Lys	Glu	Ala	Asn	Ser	Lys	Glu	Ser
				815										825
Phe	Ala	Phe	Lys	Pro	Glu	Asn	Ile	Ser	Glu	Glu	Asn	Ala	Thr	His
				830										840
Ile	Phe	Ile	Ala	Ile	Lys	Ser	Ile	Asp	Lys	Ser	Asn	Leu	Thr	Ser
				845										855
Lys	Val	Ser	Asn	Ile	Ala	Gln	Val	Thr	Leu	Phe	Ile	Pro	Gln	Ala
				860										870
Asn	Pro	Asp	Asp	Ile	Asp	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro
				875										885
Thr	Pro	Asp	Lys	Ser	His	Asn	Ser	Gly	Val	Asn	Ile	Ser	Thr	Leu
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Ser Thr Thr Ile

<210> 380  
<211> 3877  
<212> DNA  
<213> Homo sapiens

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caatcacgct ccttacacgg cctctgattt catagaagg atctaccgaa 1300

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gaaagtgaat aatgaaaagc tcaacatggc caacacgctt atcaatgtta 1450  
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 <211> 532  
 <212> PRT  
 <213> Homo sapiens

<400> 381  
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 Met Leu Ala Cys Thr Pro Lys Gly Asp Glu Glu Gln Leu Ala Leu  
 35 40 45  
 Pro Arg Ala Asn Ser Pro Thr Gly Lys Glu Gly Tyr Gln Ala Val  
 50 55 60  
 Leu Gln Glu Trp Glu Glu Gln His Arg Asn Tyr Val Ser Ser Leu  
 65 70 75  
 Lys Arg Gln Ile Ala Gln Leu Lys Glu Glu Leu Gln Glu Arg Ser  
 80 85 90

Glu	Gln	Leu	Arg	Asn	Gly	Gln	Tyr	Gln	Ala	Ser	Asp	Ala	Ala	Gly	
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Leu	Gly	Leu	Asp	Arg	Ser	Pro	Pro	Glu	Lys	Thr	Gln	Ala	Asp	Leu	
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Leu	Ala	Phe	Leu	His	Ser	Gln	Val	Asp	Lys	Ala	Glu	Val	Asn	Ala	
				125					130					135	
Gly	Val	Lys	Leu	Ala	Thr	Glu	Tyr	Ala	Ala	Val	Pro	Phe	Asp	Ser	
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Phe	Thr	Leu	Gln	Lys	Val	Tyr	Gln	Leu	Glu	Thr	Gly	Leu	Thr	Arg	
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His	Pro	Glu	Glu	Lys	Pro	Val	Arg	Lys	Asp	Lys	Arg	Asp	Glu	Leu	
				170					175					180	
Val	Glu	Ala	Ile	Glu	Ser	Ala	Leu	Glu	Thr	Leu	Asn	Asn	Pro	Ala	
				185					190					195	
Glu	Asn	Ser	Pro	Asn	His	Arg	Pro	Tyr	Thr	Ala	Ser	Asp	Phe	Ile	
				200					205					210	
Glu	Gly	Ile	Tyr	Arg	Thr	Glu	Arg	Asp	Lys	Gly	Thr	Leu	Tyr	Glu	
				215					220					225	
Leu	Thr	Phe	Lys	Gly	Asp	His	Lys	His	Glu	Phe	Lys	Arg	Leu	Ile	
				230					235					240	
Leu	Phe	Arg	Pro	Phe	Ser	Pro	Ile	Met	Lys	Val	Lys	Asn	Glu	Lys	
				245					250					255	
Leu	Asn	Met	Ala	Asn	Thr	Leu	Ile	Asn	Val	Ile	Val	Pro	Leu	Ala	
				260					265					270	
Lys	Arg	Val	Asp	Lys	Phe	Arg	Gln	Phe	Met	Gln	Asn	Phe	Arg	Glu	
				275					280					285	
Met	Cys	Ile	Glu	Gln	Asp	Gly	Arg	Val	His	Leu	Thr	Val	Val	Tyr	
				290					295					300	
Phe	Gly	Lys	Glu	Glu	Ile	Asn	Glu	Val	Lys	Gly	Ile	Leu	Glu	Asn	
				305					310					315	
Thr	Ser	Lys	Ala	Ala	Asn	Phe	Arg	Asn	Phe	Thr	Phe	Ile	Gln	Leu	
				320					325					330	
Asn	Gly	Glu	Phe	Ser	Arg	Gly	Lys	Gly	Leu	Asp	Val	Gly	Ala	Arg	
				335					340					345	
Phe	Trp	Lys	Gly	Ser	Asn	Val	Leu	Leu	Phe	Phe	Cys	Asp	Val	Asp	
				350					355					360	
Ile	Tyr	Phe	Thr	Ser	Glu	Phe	Leu	Asn	Thr	Cys	Arg	Leu	Asn	Thr	
				365					370					375	
Gln	Pro	Gly	Lys	Lys	Val	Phe	Tyr	Pro	Val	Leu	Phe	Ser	Gln	Tyr	
				380					385					390	
Asn	Pro	Gly	Ile	Ile	Tyr	Gly	His	His	Asp	Ala	Val	Pro	Pro	Leu	
				395					400					405	

Glu	Gln	Gln	Leu	Val	Ile	Lys	Lys	Glu	Thr	Gly	Phe	Trp	Arg	Asp	
				410					415					420	
Phe	Gly	Phe	Gly	Met	Thr	Cys	Gln	Tyr	Arg	Ser	Asp	Phe	Ile	Asn	
				425					430					435	
Ile	Gly	Gly	Phe	Asp	Leu	Asp	Ile	Lys	Gly	Trp	Gly	Gly	Glu	Asp	
				440					445					450	
Val	His	Leu	Tyr	Arg	Lys	Tyr	Leu	His	Ser	Asn	Leu	Ile	Val	Val	
				455					460					465	
Arg	Thr	Pro	Val	Arg	Gly	Leu	Phe	His	Leu	Trp	His	Glu	Lys	Arg	
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Cys	Met	Asp	Glu	Leu	Thr	Pro	Glu	Gln	Tyr	Lys	Met	Cys	Met	Gln	
				485					490					495	
Ser	Lys	Ala	Met	Asn	Glu	Ala	Ser	His	Gly	Gln	Leu	Gly	Met	Leu	
				500					505					510	
Val	Phe	Arg	His	Glu	Ile	Glu	Ala	His	Leu	Arg	Lys	Gln	Lys	Gln	
				515					520					525	
Lys	Thr	Ser	Ser	Lys	Lys	Thr									
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<210> 382

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

ctcggggaaa gggacttgat gttgg 25

<210> 383

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gcgaaggtga gcctctatct cgtgcc 26

<210> 384

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 384

cagcctacac gtattgagg 19

<210> 385

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 385

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<210> 386

<211> 1346

<212> DNA

<213> Homo sapiens

<400> 386

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gaacagctct gggagataaa gcatatgcct gggataccaa tgaagaatac 150  
ctcttcaaag cgatggtagc tttctccatg agaaaagttc ccaacagaga 200  
agcaacagaa atttcccatg tctactttg caatgtaacc cagagggtat 250  
cattctgggt tgtgggtaca gacccttcaa aaaatcacac ccttcctgct 300  
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<210> 387

<211> 212

<212> PRT

<213> Homo sapiens

<400> 387

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Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn  
35 40 45

Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys  
50 55 60

Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys  
65 70 75

Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp Pro  
80 85 90

Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile  
95 100 105

Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp  
110 115 120

Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro  
125 130 135

Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile  
140 145 150

Phe Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly  
155 160 165

Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp  
170 175 180

Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile Glu Asn Gly  
185 190 195

Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly Ile Leu Met Met  
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Pro Ser

<210> 388

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 388

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 cccacctgat gttgatgggg tgatagggga gatccggctc agcgtcgtgc 550  
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 gcctgtgcac tgatgatcat aatagtaatt gtagtgggtcc tcttccagca 650  
 ttaccggaaa aagcgatggg ccgaaagagc tcataaagtg gtggagataa 700  
 aatcaaaaga agaggaaagg ctcaaccaag agaaaaaggt ctctgtttat 750  
 ttagaagaca cagactaaca attttagatg gaagctgaga tgatttccaa 800  
 gaacaagaac cctagtatth cttgaagtta atggaaactt ttctttgggt 850  
 tttccagttg tgacctgttt tccaaccagt tctgcagcat attagattct 900  
 agacaagcaa caccctctg gagccagcac agtgctcctc catatcacca 950  
 gtcatacaca gcctcattat taaggctctta ttttaatttca gagtgtaaat 1000  
 tttttcaagt gctcattagg ttttataaac aagaagctac atttttgccc 1050  
 ttaagacact acttacagtg ttatgacttg tatacacata tattgggtatc 1100  
 aaaggggata aaagccaatt tgtctgttac atttcctttc acgtattttct 1150  
 tttagcagca cttctgtctac taaagttaat gtgtttactc tctttccttc 1200  
 ccacattctc aattaaaagg tgagctaagc ctctcggtg tttctgatta 1250  
 acagtaaata ctaaattcaa actgttaaata gacattttta tttttatgtc 1300  
 tctccttaac tatgagacac atcttgtttt actgaatttc tttcaatatt 1350  
 ccaggtgata gatttttgtc g 1371

<210> 389  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens

<400> 389  
 Met Tyr Gly Lys Ser Ser Thr Arg Ala Val Leu Leu Leu Leu Gly  
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Ile	Gln	Leu	Thr	Ala	Leu	Trp	Pro	Ile	Ala	Ala	Val	Glu	Ile	Tyr	
		20							25					30	
Thr	Ser	Arg	Val	Leu	Glu	Ala	Val	Asn	Gly	Thr	Asp	Ala	Arg	Leu	
			35						40					45	
Lys	Cys	Thr	Phe	Ser	Ser	Phe	Ala	Pro	Val	Gly	Asp	Ala	Leu	Thr	
				50					55					60	
Val	Thr	Trp	Asn	Phe	Arg	Pro	Leu	Asp	Gly	Gly	Pro	Glu	Gln	Phe	
				65					70					75	
Val	Phe	Tyr	Tyr	His	Ile	Asp	Pro	Phe	Gln	Pro	Met	Ser	Gly	Arg	
				80					85					90	
Phe	Lys	Asp	Arg	Val	Ser	Trp	Asp	Gly	Asn	Pro	Glu	Arg	Tyr	Asp	
				95					100					105	
Ala	Ser	Ile	Leu	Leu	Trp	Lys	Leu	Gln	Phe	Asp	Asp	Asn	Gly	Thr	
				110					115					120	
Tyr	Thr	Cys	Gln	Val	Lys	Asn	Pro	Pro	Asp	Val	Asp	Gly	Val	Ile	
				125					130					135	
Gly	Glu	Ile	Arg	Leu	Ser	Val	Val	His	Thr	Val	Arg	Phe	Ser	Glu	
				140					145					150	
Ile	His	Phe	Leu	Ala	Leu	Ala	Ile	Gly	Ser	Ala	Cys	Ala	Leu	Met	
				155					160					165	
Ile	Ile	Ile	Val	Ile	Val	Val	Val	Leu	Phe	Gln	His	Tyr	Arg	Lys	
				170					175					180	
Lys	Arg	Trp	Ala	Glu	Arg	Ala	His	Lys	Val	Val	Glu	Ile	Lys	Ser	
				185					190					195	
Lys	Glu	Glu	Glu	Arg	Leu	Asn	Gln	Glu	Lys	Lys	Val	Ser	Val	Tyr	
				200					205					210	
Leu	Glu	Asp	Thr	Asp											
				215											

<210> 390  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 390  
 ccgaggccat ctagaggcca gagc 24

<210> 391  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 391  
 acaggcagag ccaatggcca gagc 24

<210> 392  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 392  
gagaggactg cgggagtttg ggacctttgt gcagacgtgc tcatg 45

<210> 393  
<211> 471  
<212> DNA  
<213> Homo sapiens

<400> 393  
gcatttttgt ctgtgctccc tgatcttcag gtcaccacca tgaagttctt 50  
agcagtcctg gtactcttgg gagtttccat ctttctggtc tctgcccaga 100  
atccgacaac agctgctcca gctgacacgt atccagctac tggctcctgct 150  
gatgatgaag cccctgatgc tgaaaccact gctgctgcaa ccactgcgac 200  
cactgctgct cctaccactg caaccacgcg tgcttctacc actgctcgta 250  
aagacattcc agttttaccc aaatgggttg gggatctccc gaatggtaga 300  
gtgtgtccct gagatggaat cagcttgagt cttctgcaat tggtcacaac 350  
tattcatgct tcctgtgatt tcatccaact acttaccttg cctacgatat 400  
ccccctttatc tctaatacgt ttattttctt tcaaataaaa aataactatg 450  
agcaacataa aaaaaaaaaa a 471

<210> 394  
<211> 90  
<212> PRT  
<213> Homo sapiens

<400> 394  
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe  
1 5 10 15  
Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr  
20 25 30  
Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu  
35 40 45  
Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr  
50 55 60  
Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val  
65 70 75  
Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro  
80 85 90

<210> 395  
<211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 395  
gctccctgat cttcatgtca ccacc 25

<210> 396  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
cagggacaca ctctaccatt cgggag 26

<210> 397  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
ccatcttttct ggtctctgcc cagaatccga caacagctgc tc 42

<210> 398  
<211> 907  
<212> DNA  
<213> Homo sapiens

<400> 398  
ggactctgaa ggtcccaagc agctgctgag gcccccaagg aagtgggttc 50  
aaaccttgga cctaggggt ctggatttgc tggttaacaa gataacctga 100  
gggcaggacc ccatagggga atgctacctc ctgcccttcc acctgccctg 150  
gtgttcaagg tggcctggtc cctccttgcc gagagagtgt cctgggtcag 200  
ggaogcagag gacgctcaca gactccagcc ctttgttacc gagaggacac 250  
ttggcaaggt ccagcgatgg tccggagtcc acacacagac tggcggcagg 300  
gcaggagggg gacagttctg ttgtgcttgg ttggacagta agaggggtctt 350  
ggccagtcca ggggtggggg cggcaaactc cataaagaac cagaggggtct 400  
gggccccggc cacagagtca tctgccagc tcctctgctg ctggccagtg 450  
ggagtggcac gaggtggggc tttgtgccag taaaaccaca ggctggattt 500  
gcctgcgggc catgggtccct gtctagggca gcaattctca accttcttgc 550  
tctcaggacc ccaaagagct ttcattgtat ctattgattt ttaccacatt 600  
agcaattaaa actgagaaat gggccgggca cgggtggctca cgctgtaat 650

cccagcactt tgggaggccg aggcgggtgg atcacctgag atcaggagtt 700  
 caagaccagc ctggccaaca tgggtgaaacc ttgtctacta aaaatacaaa 750  
 aaattagcca ggcacagtgg tgtgcactgg tagtcccagt tactcgggag 800  
 gctgaggcag gaaaatcgct tgaacccagg aggcggacgt tgcggtgagc 850  
 cgagatcgcg ccgctgattc cagcctgggc gacaagagtg agactccatc 900  
 tcacaca 907

<210> 399  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 399  
 Met Leu Pro Pro Ala Leu Pro Pro Ala Leu Val Phe Thr Val Ala  
 1 5 10 15  
 Trp Ser Leu Leu Ala Glu Arg Val Ser Trp Val Arg Asp Ala Glu  
 20 25 30  
 Asp Ala His Arg Leu Gln Pro Phe Val Thr Glu Arg Thr Leu Gly  
 35 40 45  
 Lys Val Gln Arg Trp Ser Gly Val His Thr Gln Thr Gly Gly Arg  
 50 55 60  
 Ala Gly Gly Gly Gln Phe Cys Cys Ala Trp Leu Asp Ser Lys Arg  
 65 70 75  
 Val Leu Ala Ser Pro Gly Trp Gly Ala Ala Asn Ser Ile Lys Asn  
 80 85 90  
 Gln Arg Val Trp Ala Pro Ala Thr Glu Ser Ser Ala Gln Leu Leu  
 95 100 105  
 Cys Cys Trp Pro Val Gly Val Ala Arg Gly Gly Ala Leu Cys Gln  
 110 115 120

<210> 400  
 <211> 893  
 <212> DNA  
 <213> Homo sapiens

<400> 400  
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 ccggcctgcc tcagcggccc ccatgggcgg ccagaactg gcacagcatg 100  
 aggagctgac cctgctcttc catgggaccc tgcagctggg ccaggccctc 150  
 aacggtgtgt acaggaccac ggagggacgg ctgacaaagg ccaggaacag 200  
 cctgggtctc tatggcgcga caatagaact cctggggcag gaggtcagcc 250  
 ggggcgcggga tgcagcccag gaacttcggg caagcctgtt ggagactcag 300  
 atggaggagg atattctgca gctgcaggca gaggccacag ctgaggtgct 350  
 gggggagggtg gcccaggcac agaaggtgct acgggacagc gtgcagcggc 400

tagaagtcca gctgaggagc gcctggetgg gccctgcta ccgagaattt 450  
 gaggtcttaa aggtcacgc tgacaagcag agccacatcc tatgggccct 500  
 cacaggccac gtgcagcggc agaggcggga gatggtggca cagcagcatc 550  
 ggctgcgaca gatccaggag agactccaca cagcggcget cccagcctga 600  
 atctgcctgg atggaactga ggaccaatca tgctgcaagg aacacttcca 650  
 cgccccgtga ggccccctgtg cagggaggag ctgcctgttc actgggatca 700  
 gccagggcgc cgggccccac ttctgagcac agagcagaga cagacgcagg 750  
 cggggacaaa ggagaggat gtagcccat tggggagggg tggaggaagg 800  
 acatgtaccc tttcatgcct acacaccct cattaaagca gagtcgtggc 850  
 atttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 893

<210> 401

<211> 198

<212> PRT

<213> Homo sapiens

<400> 401

Met	Pro	Val	Pro	Ala	Leu	Cys	Leu	Leu	Trp	Ala	Leu	Ala	Met	Val
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Thr	Arg	Pro	Ala	Ser	Ala	Ala	Pro	Met	Gly	Gly	Pro	Glu	Leu	Ala
				20					25					30
Gln	His	Glu	Glu	Leu	Thr	Leu	Leu	Phe	His	Gly	Thr	Leu	Gln	Leu
				35					40					45
Gly	Gln	Ala	Leu	Asn	Gly	Val	Tyr	Arg	Thr	Thr	Glu	Gly	Arg	Leu
				50					55					60
Thr	Lys	Ala	Arg	Asn	Ser	Leu	Gly	Leu	Tyr	Gly	Arg	Thr	Ile	Glu
				65					70					75
Leu	Leu	Gly	Gln	Glu	Val	Ser	Arg	Gly	Arg	Asp	Ala	Ala	Gln	Glu
				80					85					90
Leu	Arg	Ala	Ser	Leu	Leu	Glu	Thr	Gln	Met	Glu	Glu	Asp	Ile	Leu
				95					100					105
Gln	Leu	Gln	Ala	Glu	Ala	Thr	Ala	Glu	Val	Leu	Gly	Glu	Val	Ala
				110					115					120
Gln	Ala	Gln	Lys	Val	Leu	Arg	Asp	Ser	Val	Gln	Arg	Leu	Glu	Val
				125					130					135
Gln	Leu	Arg	Ser	Ala	Trp	Leu	Gly	Pro	Ala	Tyr	Arg	Glu	Phe	Glu
				140					145					150
Val	Leu	Lys	Ala	His	Ala	Asp	Lys	Gln	Ser	His	Ile	Leu	Trp	Ala
				155					160					165
Leu	Thr	Gly	His	Val	Gln	Arg	Gln	Arg	Arg	Glu	Met	Val	Ala	Gln
				170					175					180
Gln	His	Arg	Leu	Arg	Gln	Ile	Gln	Glu	Arg	Leu	His	Thr	Ala	Ala

Leu Pro Ala

<210> 402  
<211> 1915  
<212> DNA  
<213> Homo sapiens

<400> 402  
ggcaacatgg ctcagcaggc ttgccccaga gccatggcaa agaatggact 50  
tgtaatttgc atcctggtga tcaccttact cctggaccag accaccagcc 100  
acacatccag attaaaagcc aggaagcaca gcaaacgtcg agtgagagac 150  
aaggatggag atctgaagac tcaaattgaa aagctctgga cagaagtcaa 200  
tgccttgaag gaaattcaag ccctgcagac agtctgtctc cgaggcacta 250  
aagttcacaa gaaatgctac cttgcttcag aaggtttgaa gcatttccat 300  
gaggccaatg aagactgcat ttccaaagga ggaatcctgg ttatccccag 350  
gaactccgac gaaatcaacg ccctccaaga ctatggtaaa aggagcctgc 400  
cagggtgtcaa tgacttttgg ctgggcatca atgacatggc cacggaaggc 450  
aagtttgttg acgtcaacgg aatcgctatc tccttcctca actgggaccg 500  
tgcacagcct aacggtggca agcgagaaaa ctgtgtcctg ttctcccaat 550  
cagctcaggg caagtggagt gatgaggcct gtgcgcagcag caagagatac 600  
atatgcgagt tcaccatccc taaataggtc tttctccaat gtgtcctcca 650  
agcaagattc atcataactt ataggttcat gatctctaag atcaagtaaa 700  
aatcataatt tttacttatt aaaaaattgc aacacaagat caatgtccat 750  
agcaatatga tagcatcagc caattttgct aacacatttc tttgggattt 800  
tgcccttcct ggggtatagg ggalcagaaa tattgatcca tgtgcacgca 850  
gataaaatgg cttctgctaa acagactaaa atctttctct ctagtctttc 900  
tcacttgtac aaaccagtt tgttttcaaa aaatcacagt agcaatgcaa 950  
ctcatcactc tagaaaagca agcttaggct acctgaaaga ttttcccttg 1000  
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aggtgctata taatccaaaa acttttcagc ctgttgctca ttctgtccca 1100  
tgctggcaat aataccttgt cagccatta cccttatttt gaattgctcc 1150  
atctcctggg gggacttgta tcttgtctgc catatcagaa cacaaacccc 1200  
tgaagaggtt ctgatttgat tttttttttt tottcatgcc tacccttttt 1250  
ttggaagttt ccagccgcaa tttgaaatga aatgacaagg tgtatatttg 1300

atcaattttc attcccacca ttgcattaca acctctaact taaatgggta 1350  
 accctaaggc atatcaaaga agcagattgc atgataaacg gaaatagaaa 1400  
 aaaagaacct acattttattt tgcttttagca tccttactct caccttttat 1450  
 gagattgaga gtggacttac atttcctttt ttacattttc gtatatttat 1500  
 ttttttttagc catcattata tgtttaagtc tattatgggc aaccaatctt 1550  
 tgggaagctga aaactgaatt taaagaatgc tatcttggaa aattgcatac 1600  
 gtctgtgcaa ttttttattc tgcctagtagc tattctgctt gtttaactag 1650  
 attgtacaaa ataacttcat tgcttaatat caaattacaa agtttagact 1700  
 tggaggggaaa tgggctttttt agaagcaaac aatttttaa atattttgtt 1750  
 cttcaaataa atagtgttta aacattgaat gtgttttgtg aacaatatcc 1800  
 cactttgcaa actttaacta cacatgcttg gaattaagtt ttagctgttt 1850  
 tcattgctca ataataaagc ctgaattctg atcaataaaa aaaaaaaaaa 1900  
 aaaaaaaaaa aaaaa 1915

<210> 403  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

<400> 403  
 Met Ala Gln Gln Ala Cys Pro Arg Ala Met Ala Lys Asn Gly Leu  
 1 5 10 15  
 Val Ile Cys Ile Leu Val Ile Thr Leu Leu Leu Asp Gln Thr Thr  
 20 25 30  
 Ser His Thr Ser Arg Leu Lys Ala Arg Lys His Ser Lys Arg Arg  
 35 40 45  
 Val Arg Asp Lys Asp Gly Asp Leu Lys Thr Gln Ile Glu Lys Leu  
 50 55 60  
 Trp Thr Glu Val Asn Ala Leu Lys Glu Ile Gln Ala Leu Gln Thr  
 65 70 75  
 Val Cys Leu Arg Gly Thr Lys Val His Lys Lys Cys Tyr Leu Ala  
 80 85 90  
 Ser Glu Gly Leu Lys His Phe His Glu Ala Asn Glu Asp Cys Ile  
 95 100 105  
 Ser Lys Gly Gly Ile Leu Val Ile Pro Arg Asn Ser Asp Glu Ile  
 110 115 120  
 Asn Ala Leu Gln Asp Tyr Gly Lys Arg Ser Leu Pro Gly Val Asn  
 125 130 135  
 Asp Phe Trp Leu Gly Ile Asn Asp Met Val Thr Glu Gly Lys Phe  
 140 145 150  
 Val Asp Val Asn Gly Ile Ala Ile Ser Phe Leu Asn Trp Asp Arg

	155		160		165
Ala Gln Pro Asn Gly Gly Lys Arg Glu Asn Cys Val Leu Phe Ser	170		175		180
Gln Ser Ala Gln Gly Lys Trp Ser Asp Glu Ala Cys Arg Ser Ser	185		190		195
Lys Arg Tyr Ile Cys Glu Phe Thr Ile Pro Lys	200		205		

<210> 404  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 404  
 cctgggtatc cccaggaact ccgac 25

<210> 405  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 405  
 ctcttgctgc tgcgacaggc etc 23

<210> 406  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 406  
 cgccctccaa gactatggta aaaggagcct gccaggtgtc aatgac 46

<210> 407  
 <211> 570  
 <212> DNA  
 <213> Homo sapiens

<400> 407  
 gcgaggaccg ggtataagaa gcctcgtggc cttgcccggg cagccgcagg 50  
 ttccccgcgc gccccgagcc cccgcgccat gaagctcgcc gccctcctgg 100  
 ggctctgcgt ggccctgtcc tgcagctccg ctgctgcttt cttagtgggc 150  
 tcggccaagc ctgtggccca gcctgtcgct gcgctggagt cggcggcgga 200  
 ggccggggcc gggaccctgg ccaaccccct cggcaccctc aaccgcgtga 250  
 agctcctgct gaggagcctg ggcatccccg tgaaccacct catagagggc 300  
 tcccagaagt gtgtggctga gctgggtccc caggccgtgg gggccgtgaa 350

ggccctgaag gccctgctgg gggccctgac agtgtttggc tgagccgaga 400  
 ctggagcatc tacacctgag gacaagacgc tgcccacccg cgaggggtga 450  
 aaaccccgcc gcggggagga cctgccatcc cttccccccg gcccctctca 500  
 ataaacgtgg ttaagagcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550  
 aaaaaaaaaa aaaaaaaaaa 570

<210> 408  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 408  
 Met Lys Leu Ala Ala Leu Leu Gly Leu Cys Val Ala Leu Ser Cys  
     1                    5                    10                    15  
 Ser Ser Ala Ala Ala Phe Leu Val Gly Ser Ala Lys Pro Val Ala  
                     20                    25                    30  
 Gln Pro Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly Ala Gly  
                     35                    40                    45  
 Thr Leu Ala Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys Leu Leu  
                     50                    55                    60  
 Leu Ser Ser Leu Gly Ile Pro Val Asn His Leu Ile Glu Gly Ser  
                     65                    70                    75  
 Gln Lys Cys Val Ala Glu Leu Gly Pro Gln Ala Val Gly Ala Val  
                     80                    85                    90  
 Lys Ala Leu Lys Ala Leu Leu Gly Ala Leu Thr Val Phe Gly  
                     95                    100

<210> 409  
 <211> 2089  
 <212> DNA  
 <213> Homo sapiens

<400> 409  
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 aaggaggcca ctccctggcc tccgcagccg atcacatgaa ggtggtgcca 100  
 agtctcctgc tctccgtcct cctggcacag gtgtggctgg taccggcctt 150  
 ggcccccagt cctcagtcgc cagagacccc agcccctcag aaccagacca 200  
 gcagggtagt gcaggctccc agggaggaag aggaagatga gcaggaggcc 250  
 agcgaggaga aggcgggtga ggaagagaaa gcctggctga tggccagcag 300  
 gcagcagctt gccaaaggaga cttcaaactt cggattcagc ctgctgcgaa 350  
 agatctocat gaggaacgat ggcaacatgg tcttctctcc atttggcatg 400  
 tccttggcca tgacaggctt gatgctgggg gccacagggc cgactgaaac 450  
 ccagatcaag agagggctcc acttgcaggc cctgaagccc accaagcccg 500

ggctcctgcc ttccctcttt aagggactca gagagaccct ctcccgaac 550  
 ctggaactgg gcctctcaca ggggagtttt gccttcatcc acaaggattt 600  
 tgatgtcaaa gagactttct tcaattttatc caagaggtat ttgatacag 650  
 agtgcgtgcc tatgaatttt cgcaatgcct cacaggccaa aaggctcatg 700  
 aatcattaca ttaacaaaga gactcggggg aaaattccca aactgtttga 750  
 tgagattaat cctgaaacca aattaattct tgtggattac atcttggtca 800  
 aagggaaatg gttgacccca ttgaccctg tcttcaccga agtcgacact 850  
 ttccacctgg acaagtacaa gaccattaag gtgcccatga tgtacggtgc 900  
 aggcaagttt gcctccacct ttgacaagaa ttttcgttgt catgtcctca 950  
 aactgcccta ccaaggaaat gccaccatgc tgggtggtcct catggagaaa 1000  
 atgggtgacc acctcgccct tgaagactac ctgaccacag acttggtgga 1050  
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 agttcaagct agatcagaag tatgagatgc atgagctgct taggcagatg 1150  
 ggaatcagaa gaatcttctc accctttgct gaccttagtg aactctcagc 1200  
 tactggaaga aatctccaag tatccagggt tttaacgaaga acagtgattg 1250  
 aagttgatga aaggggcact gaggcagtgg caggaatctt gtcagaaatt 1300  
 actgcttatt ccatgcctcc tgtcatcaaa gtggacgggc catttcattt 1350  
 catgatctat gaagaaacct ctggaatgct tctgtttctg ggcagggtgg 1400  
 tgaatccgac tctcctataa ttcaggacat gcataagcac ttcgtgctgt 1450  
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 atggcagggg agagtgttcc ttttgttctt aactagttta ggggtgttctc 1550  
 aaataaatac agtagtcccc acttatctga gggggataca ttcaaagacc 1600  
 cccagcagat gcctgaaacg gtggacagtg ctgaacctta tatatatttt 1650  
 ttcttacaca tacataccta tgataaagtt taatttataa attaggcaca 1700  
 gtaagagatt aacaataata acaacattaa gtaaaatgag ttacttgaac 1750  
 gcaagcactg caataccata acagtcaaac tgattataga gaaggctact 1800  
 aagtgactca tgggcgagga gcatagacag tgtggagaca ttgggcaagg 1850  
 ggagaattca catcctgggt gggacagagc aggacgatgc aagattccat 1900  
 cccactactc agaatggcat gctgcttaag acttttagat tgtttatttc 1950  
 tggaattttt catttaatgt ttttgacca tggttgacca tggttaactg 2000  
 agactgcaga aagcaaaacc atggataagg gaggactact acaaaagcat 2050  
 taaattgata catatttttt aaaaaaaaaa aaaaaaaaaa 2089

<210> 410  
 <211> 444  
 <212> PRT  
 <213> Homo sapiens

<400> 410

Met	Lys	Val	Val	Pro	Ser	Leu	Leu	Leu	Ser	Val	Leu	Leu	Ala	Gln	1	5	10	15
Val	Trp	Leu	Val	Pro	Gly	Leu	Ala	Pro	Ser	Pro	Gln	Ser	Pro	Glu	20	25	30	
Thr	Pro	Ala	Pro	Gln	Asn	Gln	Thr	Ser	Arg	Val	Val	Gln	Ala	Pro	35	40	45	
Arg	Glu	Glu	Glu	Glu	Asp	Glu	Gln	Glu	Ala	Ser	Glu	Glu	Lys	Ala	50	55	60	
Gly	Glu	Glu	Glu	Lys	Ala	Trp	Leu	Met	Ala	Ser	Arg	Gln	Gln	Leu	65	70	75	
Ala	Lys	Glu	Thr	Ser	Asn	Phe	Gly	Phe	Ser	Leu	Leu	Arg	Lys	Ile	80	85	90	
Ser	Met	Arg	His	Asp	Gly	Asn	Met	Val	Phe	Ser	Pro	Phe	Gly	Met	95	100	105	
Ser	Leu	Ala	Met	Thr	Gly	Leu	Met	Leu	Gly	Ala	Thr	Gly	Pro	Thr	110	115	120	
Glu	Thr	Gln	Ile	Lys	Arg	Gly	Leu	His	Leu	Gln	Ala	Leu	Lys	Pro	125	130	135	
Thr	Lys	Pro	Gly	Leu	Leu	Pro	Ser	Leu	Phe	Lys	Gly	Leu	Arg	Glu	140	145	150	
Thr	Leu	Ser	Arg	Asn	Leu	Glu	Leu	Gly	Leu	Ser	Gln	Gly	Ser	Phe	155	160	165	
Ala	Phe	Ile	His	Lys	Asp	Phe	Asp	Val	Lys	Glu	Thr	Phe	Phe	Asn	170	175	180	
Leu	Ser	Lys	Arg	Tyr	Phe	Asp	Thr	Glu	Cys	Val	Pro	Met	Asn	Phe	185	190	195	
Arg	Asn	Ala	Ser	Gln	Ala	Lys	Arg	Leu	Met	Asn	His	Tyr	Ile	Asn	200	205	210	
Lys	Glu	Thr	Arg	Gly	Lys	Ile	Pro	Lys	Leu	Phe	Asp	Glu	Ile	Asn	215	220	225	
Pro	Glu	Thr	Lys	Leu	Ile	Leu	Val	Asp	Tyr	Ile	Leu	Phe	Lys	Gly	230	235	240	
Lys	Trp	Leu	Thr	Pro	Phe	Asp	Pro	Val	Phe	Thr	Glu	Val	Asp	Thr	245	250	255	
Phe	His	Leu	Asp	Lys	Tyr	Lys	Thr	Ile	Lys	Val	Pro	Met	Met	Tyr	260	265	270	
Gly	Ala	Gly	Lys	Phe	Ala	Ser	Thr	Phe	Asp	Lys	Asn	Phe	Arg	Cys	275	280	285	

His	Val	Leu	Lys	Leu	Pro	Tyr	Gln	Gly	Asn	Ala	Thr	Met	Leu	Val	290	295	300
Val	Leu	Met	Glu	Lys	Met	Gly	Asp	His	Leu	Ala	Leu	Glu	Asp	Tyr	305	310	315
Leu	Thr	Thr	Asp	Leu	Val	Glu	Thr	Trp	Leu	Arg	Asn	Met	Lys	Thr	320	325	330
Arg	Asn	Met	Glu	Val	Phe	Phe	Pro	Lys	Phe	Lys	Leu	Asp	Gln	Lys	335	340	345
Tyr	Glu	Met	His	Glu	Leu	Leu	Arg	Gln	Met	Gly	Ile	Arg	Arg	Ile	350	355	360
Phe	Ser	Pro	Phe	Ala	Asp	Leu	Ser	Glu	Leu	Ser	Ala	Thr	Gly	Arg	365	370	375
Asn	Leu	Gln	Val	Ser	Arg	Val	Leu	Arg	Arg	Thr	Val	Ile	Glu	Val	380	385	390
Asp	Glu	Arg	Gly	Thr	Glu	Ala	Val	Ala	Gly	Ile	Leu	Ser	Glu	Ile	395	400	405
Thr	Ala	Tyr	Ser	Met	Pro	Pro	Val	Ile	Lys	Val	Asp	Arg	Pro	Phe	410	415	420
His	Phe	Met	Ile	Tyr	Glu	Glu	Thr	Ser	Gly	Met	Leu	Leu	Phe	Leu	425	430	435
Gly	Arg	Val	Val	Asn	Pro	Thr	Leu	Leu							440		

<210> 411  
 <211> 636  
 <212> DNA  
 <213> Homo sapiens

<400> 411  
 ctgggatcag ccactgcagc tccctgagca ctctctacag agacgcggac 50  
 cccagacatg aggaggctcc tccctggcac cagcctggtg gttgtgctgc 100  
 tgtgggaggc aggtgcagtc ccagcaccca aggtccctat caagatgcaa 150  
 gtcaaacact ggccctcaga gcaggaccca gagaaggcct ggggcgcccg 200  
 tgtggtggag cctccggaga aggacgacca gctggtggtg ctgttccctg 250  
 tccagaagcc gaaactcttg accaccgagg agaagccacg aggtcagggc 300  
 aggggccccca tccttcagg caccaaggcc tggatggaga ccgaggacac 350  
 cctgggcoct gtccctgagtc ccgagcccga ccatgacagc ctgtaccacc 400  
 ctccgcctga ggaggaccag ggcgaggaga ggccccggtt gtgggtgatg 450  
 ccaaatacc aggtgctcct gggaccggag gaagaccaag accacatcta 500  
 ccacccccag tagggctcca ggggccatca ctgccccgc cctgtcccaa 550  
 ggcccaggct gttgggactg ggaccctccc taccctgcc cagctagaca 600

aataaacccc agcaggcaaa aaaaaaaaaa aaaaaa 636

<210> 412  
<211> 151  
<212> PRT  
<213> Homo sapiens

<400> 412  
Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu  
1 5 10 15  
Trp Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met  
20 25 30  
Gln Val Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp  
35 40 45  
Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val  
50 55 60  
Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu  
65 70 75  
Lys Pro Arg Gly Gln Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys  
80 85 90  
Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg Val Leu Ser Pro  
95 100 105  
Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro Glu Glu Asp  
110 115 120  
Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro Asn His Gln  
125 130 135  
Val Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr His Pro  
140 145 150  
Gln

<210> 413  
<211> 1176  
<212> DNA  
<213> Homo sapiens

<400> 413  
agaaagctgc actctgttga gctccagggc gcagtggagg gagggagtga 50  
aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta 100  
caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150  
tgaggtacag atgaggctaa tacttacttc aaggaatgga cctgtttctc 200  
gtctccatct ctgcccagaa gctgcaagga aatcaaagac gaatgtccta 250  
gtgcatttga tggcctgtat ttctcgcga ctgagaatgg tggtatctac 300  
cagaccttct gtgacatgac ctctgggggt ggcggtgga ccctggtggc 350  
cagcgtgcat gagaatgaca tgcgtgggaa gtgcacggtg ggcgatcgct 400

ggtccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac 450  
 tggggccaact acaacacctt tggatctgca gagggcgcca cgagcgatga 500  
 ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct 550  
 ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagctccctg 600  
 ctgaggtacc gcacggacac tggcttcctc cagacactgg gacataatct 650  
 gtttggcatc taccagaaat atccagtga atattggagaa ggaaagtgtt 700  
 ggactgacaa cggcccgggtg atccctgtgg tctatgattt tggcgacgcc 750  
 cagaaaacag catcttatta ctcacctat ggccagcggg aattcactgc 800  
 gggatttgtt cagttcaggg tatttaataa cgagagagca gccaacgcct 850  
 tgtgtgctgg aatgaggggtc accggatgta aactgagca tcaactgcatt 900  
 ggtggaggag gatactttcc agaggccagt ccccgagcagt gtggagattt 950  
 ttctgggtttt gattggagt gatatggaac tcatgttggt tacagcagca 1000  
 gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt 1050  
 tgtgggaggg aaccagacc tctcctccca accatgagat cccaaggatg 1100  
 gagaacaact taccagtag ctagaatgtt aatggcagaa gagaaaacaa 1150  
 taaatcatat tgactcaaga aaaaaa 1176

<210> 414  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 414  
 Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg  
 1 5 10 15  
 Gly Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr  
 20 25 30  
 Cys Ser Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys  
 35 40 45  
 Asp Glu Cys Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr  
 50 55 60  
 Glu Asn Gly Val Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly  
 65 70 75  
 Gly Gly Gly Trp Thr Leu Val Ala Ser Val His Glu Asn Asp Met  
 80 85 90  
 Arg Gly Lys Cys Thr Val Gly Asp Arg Trp Ser Ser Gln Gln Gly  
 95 100 105  
 Ser Lys Ala Asp Tyr Pro Glu Gly Asp Gly Asn Trp Ala Asn Tyr  
 110 115 120  
 Asn Thr Phe Gly Ser Ala Glu Ala Ala Thr Ser Asp Asp Tyr Lys

125					130					135				
Asn	Pro	Gly	Tyr	Tyr	Asp	Ile	Gln	Ala	Lys	Asp	Leu	Gly	Ile	Trp
				140					145					150
His	Val	Pro	Asn	Lys	Ser	Pro	Met	Gln	His	Trp	Arg	Asn	Ser	Ser
				155					160					165
Leu	Leu	Arg	Tyr	Arg	Thr	Asp	Thr	Gly	Phe	Leu	Gln	Thr	Leu	Gly
				170					175					180
His	Asn	Leu	Phe	Gly	Ile	Tyr	Gln	Lys	Tyr	Pro	Val	Lys	Tyr	Gly
				185					190					195
Glu	Gly	Lys	Cys	Trp	Thr	Asp	Asn	Gly	Pro	Val	Ile	Pro	Val	Val
				200					205					210
Tyr	Asp	Phe	Gly	Asp	Ala	Gln	Lys	Thr	Ala	Ser	Tyr	Tyr	Ser	Pro
				215					220					225
Tyr	Gly	Gln	Arg	Glu	Phe	Thr	Ala	Gly	Phe	Val	Gln	Phe	Arg	Val
				230					235					240
Phe	Asn	Asn	Glu	Arg	Ala	Ala	Asn	Ala	Leu	Cys	Ala	Gly	Met	Arg
				245					250					255
Val	Thr	Gly	Cys	Asn	Thr	Glu	His	His	Cys	Ile	Gly	Gly	Gly	Gly
				260					265					270
Tyr	Phe	Pro	Glu	Ala	Ser	Pro	Gln	Gln	Cys	Gly	Asp	Phe	Ser	Gly
				275					280					285
Phe	Asp	Trp	Ser	Gly	Tyr	Gly	Thr	His	Val	Gly	Tyr	Ser	Ser	Ser
				290					295					300
Arg	Glu	Ile	Thr	Glu	Ala	Ala	Val	Leu	Leu	Phe	Tyr	Arg		
				305					310					

<210> 415  
 <211> 1281  
 <212> DNA  
 <213> Homo sapiens

<400> 415  
 gcggagccgg cgccggctgc gcagaggagc cgctctcgcc gccgccacct 50  
 cggctgggag cccacgaggc tgccgcatcc tgccctcgga acaatgggac 100  
 tcggcgcgcg aggtgcttgg gccgcgctgc tcctggggac gctgcaggtg 150  
 ctagcgctgc tggggggccgc ccatgaaagc gcagccatgg cggcatctgc 200  
 aaacatagag aattctgggc ttccacacaa ctccagtgtt aactcaacag 250  
 agactctcca acatgtgcct tctgaccata caaatgaaac ttccaacagt 300  
 actgtgaaac caccaacttc agttgcctca gactccagta atacaacggt 350  
 caccaccatg aaacctacag cggcatctaa tacaacaaca ccagggatgg 400  
 tctcaacaaa tatgacttct accaccttaa agtctacacc caaaacaaca 450  
 agtgtttcac agaacacatc tcagatatca acatccacaa tgaccgtaac 500

ccacaatagt tcagtgacat ctgctgcttc atcagtaaca atcacaacaa 550  
 ctatgcattc tgaagcaaag aaaggatcaa aatttgatac tgggagcttt 600  
 gttggtggta ttgtattaac gctgggagtt ttatctattc tttacattgg 650  
 atgcaaaatg tattactcaa gaagaggcat tcggtatcga accatagatg 700  
 aacatgatgc catcatttaa ggaaatccat ggaccaagga tggatacag 750  
 attgatgctg ccctatcaat taattttggt ttattaatag tttaaaacaa 800  
 tattctcttt ttgaaaatag tataaacagg ccatgcatat aatgtacagt 850  
 gtattacgta aatatgtaaa gattcttcaa ggtaacaagg gtttgggttt 900  
 tgaaataaac atctggatct tatagaccgt tcatacaatg gtttttagcaa 950  
 gttcatagta agacaaacaa gtcctatctt ttttttttgg ctggggtggg 1000  
 ggcattggtc acatatgacc agtaattgaa agacgtcatc actgaaagac 1050  
 agaatgccat ctgggcatac aaataagaag tttgtcacag cactcaggat 1100  
 tttgggtatc ttttgtagct cacataaaga acttcagtgc ttttcagagc 1150  
 tggatatatc ttaattacta atgccacaca gaaattatac aatcaaacta 1200  
 gatctgaagc ataatttaag aaaaacatca acattttttg tgctttaaac 1250  
 tgtagtagtt ggtctagaaa caaaatactc c 1281

<210> 416  
 <211> 208  
 <212> PRT  
 <213> Homo sapiens

<400> 416  
 Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly  
 1 5 10 15  
 Thr Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala  
 20 25 30  
 Ala Met Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His  
 35 40 45  
 Asn Ser Ser Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser  
 50 55 60  
 Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr  
 65 70 75  
 Ser Val Ala Ser Asp Ser Ser Asn Thr Thr Val Thr Thr Met Lys  
 80 85 90  
 Pro Thr Ala Ala Ser Asn Thr Thr Thr Pro Gly Met Val Ser Thr  
 95 100 105  
 Asn Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser  
 110 115 120  
 Val Ser Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val

	125		130		135
Thr His Asn Ser	Ser Val Thr Ser Ala	Ala Ser Ser Val Thr	Ile		
	140		145		150
Thr Thr Thr Met	His Ser Glu Ala Lys	Lys Gly Ser Lys Phe	Asp		
	155		160		165
Thr Gly Ser Phe	Val Gly Gly Ile Val	Leu Thr Leu Gly Val	Leu		
	170		175		180
Ser Ile Leu Tyr	Ile Gly Cys Lys Met	Tyr Tyr Ser Arg Arg	Gly		
	185		190		195
Ile Arg Tyr Arg	Thr Ile Asp Glu His	Asp Ala Ile Ile			
	200		205		

<210> 417  
 <211> 1728  
 <212> DNA  
 <213> Homo sapiens

<400> 417  
 cagccggggtc ccaagcctgt gcctgagcct gagcctgagc ctgagcccga 50  
 gccgggagcc ggtcgcgggg gtcgccgggt gtgggaccgc tgggccccca 100  
 gcgatggcga ccctgtgggg aggccttctt cggcttggtt ccttgctcag 150  
 cctgtcgtgc ctggcgcttt cctgtctgct gctggcgagc ctgtcagacg 200  
 ccgccaagaa tttcgaggat gtcagatgta aatgtatctg ccctccctat 250  
 aaagaaaatt ctgggcatat ttataataag aacatatctc agaaagattg 300  
 tgattgcctt catgttggtg agcccatgcc tgtgcggggg cctgatgtag 350  
 aagcatactg tctacgtgtg gaatgcaa atgaagaaag aagctctgtc 400  
 acaatcaagg ttaccattat aatttatctc tccatttttg gccttctact 450  
 tctgtacatg gtatatctta ctctggttga gccatactg aagaggcgcc 500  
 tcttttgaca tgcacagttg atacagagtg atgatgatat tggggatcac 550  
 cagccttttg caaatgcaca cgatgtgcta gcccgtccc gcagtcgagc 600  
 caacgtgctg aacaaggtag aatatgcaca gcagcgctgg aagcttcaag 650  
 tccaagagca gcgaaagtct gtctttgacc ggcatgttgt cctcagctaa 700  
 ttgggaattg aattcaaggt gactagaaag aaacaggcag acaactggaa 750  
 agaactgact gggttttgct gggtttcatt ttaatacctt gttgatttca 800  
 ccaactggtg ctggaagatt caaaactgga agcaaaaact tgcttgattt 850  
 ttttttcttg ttaacgtaat aatagagaca tttttaaaag cacacagctc 900  
 aaagtcagcc aataagtctt ttcctatttg tgacttttac taataaaaat 950  
 aaatctgcct gtaaattatc ttgaagtcct ttacctggaa caagcactct 1000

ctttttcacc acatagtttt aacttgactt tcaagataat tttcaggggtt 1050  
 tttgttgggtt ttgttttttg tttgtttgtt ttggtgggag aggggagggga 1100  
 tgcctgggaa gtggttaaca acttttttca agtcacttta ctaaacaac 1150  
 ttttgtaaag agaccttacc ttctattttc gagtttcatt tatattttgc 1200  
 agtgtagcca gcctcatcaa agagctgact tactcatttg acttttgcac 1250  
 tgactgtatt atctgggtat ctgctgtgtc tgcacttcat ggtaaacggg 1300  
 atctaaaatg cctgggtggct tttcacaaaa agcagatttt cttcatgtac 1350  
 tgtgatgtct gatgcaatgc atcctagaac aaactggcca tttgctagtt 1400  
 tactctaaag actaaacata gtcttggtgt gtgtggtctt actcatcttc 1450  
 tagtaccttt aaggacaaat cctaaggact tggacacttg caataaagaa 1500  
 attttatttt aaaccaagc ctccctggat tgataatata tacacatttg 1550  
 tcagcatttc cggtcgtggt gagaggcagc tgtttgagct ccaatatgtg 1600  
 cagctttgaa ctagggctgg gggtgtgggt gcctcttctg aaagggtctaa 1650  
 ccattattgg ataactggct tttttcttcc tatgtcctct ttggaatgta 1700  
 acaataaaaa taatttttga aacatcaa 1728

<210> 418  
 <211> 198  
 <212> PRT  
 <213> Homo sapiens

<400> 418  
 Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu  
 1 5 10 15  
 Ser Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu  
 20 25 30  
 Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile  
 35 40 45  
 Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn  
 50 55 60  
 Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu Pro Met  
 65 70 75  
 Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu  
 80 85 90  
 Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile  
 95 100 105  
 Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val  
 110 115 120  
 Tyr Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly  
 125 130 135

His	Ala	Gln	Leu	Ile	Gln	Ser	Asp	Asp	Asp	Ile	Gly	Asp	His	Gln
				140					145					150
Pro	Phe	Ala	Asn	Ala	His	Asp	Val	Leu	Ala	Arg	Ser	Arg	Ser	Arg
				155					160					165
Ala	Asn	Val	Leu	Asn	Lys	Val	Glu	Tyr	Ala	Gln	Gln	Arg	Trp	Lys
				170					175					180
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Ser	Val	Phe	Asp	Arg	His	Val
				185					190					195

Val Leu Ser

<210> 419  
 <211> 681  
 <212> DNA  
 <213> Homo sapiens

<400> 419  
 gcacctgcga ccacctgag cagtcattggc gtactccaca gtgcagagag 50  
 tcgctctggc ttctgggctt gtcctggctc tgctgctgct gctgcccaag 100  
 gccttcctgt cccgcgggaa gcggcaggag ccgcgcgcga cacctgaagg 150  
 aaaattgggc cgatttccac ctatgatgca tcattaccag gcacctcag 200  
 atggccagac tcctggggct cgtttccaga ggtctcacct tgccgaggca 250  
 tttgcaaagg ccaaaggatc aggtggaggt gctggaggag gaggtagtgg 300  
 aagaggtctg atggggcaga ttattccaat ctacggtttt gggatttttt 350  
 tatatatact gtacattcta ttaaggtaa gtagaatcat cctaatacata 400  
 ttacatcaat gaaaatctaa tatggcgata aaaatcattg tctacattaa 450  
 aacttcttat agttcataaa attatttcaa atccatcatc tottttaaate 500  
 ctgcctcttc ttcattgagg acttaggata gccattattt cagtttcaca 550  
 taagaatgtt tactcaatgt ttaagtgtt tgccccaaaa ttcacaacta 600  
 acaaggcaga actaggactt gaacatggat cttttggttc ttaatccagt 650  
 gattgataca attcaatgca ctcccctgcc a 681

<210> 420  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 420  
 Met Ala Tyr Ser Thr Val Gln Arg Val Ala Leu Ala Ser Gly Leu  
 1 5 10 15  
 Val Leu Ala Leu Ser Leu Leu Leu Pro Lys Ala Phe Leu Ser Arg  
 20 25 30  
 Gly Lys Arg Gln Glu Pro Pro Pro Thr Pro Glu Gly Lys Leu Gly  
 35 40 45

Arg	Phe	Pro	Pro	Met	Met	His	His	His	Gln	Ala	Pro	Ser	Asp	Gly
				50					55					60
Gln	Thr	Pro	Gly	Ala	Arg	Phe	Gln	Arg	Ser	His	Leu	Ala	Glu	Ala
			65						70					75
Phe	Ala	Lys	Ala	Lys	Gly	Ser	Gly	Gly	Gly	Ala	Gly	Gly	Gly	Gly
			80						85					90
Ser	Gly	Arg	Gly	Leu	Met	Gly	Gln	Ile	Ile	Pro	Ile	Tyr	Gly	Phe
			95						100					105
Gly	Ile	Phe	Leu	Tyr	Ile	Leu	Tyr	Ile	Leu	Phe	Lys	Val	Ser	Arg
			110						115					120
Ile	Ile	Leu	Ile	Ile	Leu	His	Gln							
			125											

<210> 421  
 <211> 1630  
 <212> DNA  
 <213> Homo sapiens

<400> 421  
 cggctcagat gcagctgtgg ggagatttca gtgcattgcc tcccctgggt 50  
 gctcttcac tttgatttga aagttgagag cagcatgttt tgcccactga 100  
 aactcactct gctgccagtg ttactggatt attccttggg cctgaatgac 150  
 ttgaatgttt ccccgctga gctaacagtc catgtgggtg attcagctct 200  
 gatgggatgt gttttccaga gcacagaaga caaatgtata ttcaagatag 250  
 actggactct gtcaccagga gagcacgcca aggacgaata tgtgctatac 300  
 tattactcca atctcagtgt gcctattggg cgcttccaga accgcgtaca 350  
 cttgatgggg gacatcttat gcaatgatgg ctctctcctg ctccaagatg 400  
 tgcaagaggc tgaccagga acctatatct gtgaaatccg cctcaaaggg 450  
 gagagccagg tgttcaagaa ggcggtggta ctgcatgtgc ttccagagga 500  
 gcccaaagag ctcatggtcc atgtgggtgg attgattcag atgggatgtg 550  
 ttttccagag cacagaagtg aaacacgtga ccaaggtaga atggatattt 600  
 tcaggacggc gcgcaaagga ggagattgta tttcgttact accacaaact 650  
 caggatgtct gtggagtact cccagagctg gggccacttc cagaatcgtg 700  
 tgaacctggt gggggacatt ttccgcaatg acggttccat catgcttcaa 750  
 ggagtgaggg agtcagatgg aggaaactac acctgcagta tccacctagg 800  
 gaacctggtg ttcaagaaaa ccattgtgct gcatgtcagc ccggaagagc 850  
 ctcgaacact ggtgaccccg gcagccctga ggcctctggt cttgggtggt 900  
 aatcagttgg tgatcattgt gggaattgtc tgtgccacaa tcctgctgct 950  
 cctgtttctg atattgatcg tgaagaagac ctgtggaaat aagagttcag 1000

tgaattctac agtcttggtg aagaacacga agaagactaa tccagagata 1050  
aaagaaaaac cctgccattht tgaaagatgt gaaggggaga aacacattta 1100  
ctccccaata attgtacggg aggtgatcga ggaagaagaa ccaagtgaaa 1150  
aatcagaggc cacctacatg accatgcacc cagtttgccc ttctctgagg 1200  
tcagatcgga acaactcact tgaaaaaaag tcaggtgggg gaatgccaaa 1250  
aacacagcaa gccttttgag aagaatggag agtcccttca tctcagcagc 1300  
gggtggagact ctctcctgtg tgtgtcctgg gccactctac cagtgatthc 1350  
agactcccgc tctccagct gtcctcctgt ctcatgtttt ggtcaatata 1400  
ctgaagatgg agaatttgga gcctggcaga gagactggac agctctggag 1450  
gaacaggcct gctgagggga ggggagcatg gacttggcct ctggagtggg 1500  
acactggccc tgggaaccag gctgagctga gtggcctcaa accccccgtt 1550  
ggatcagacc ctctgtggg cagggttctt agtggatgag ttactgggaa 1600  
gaatcagaga taaaaaccaa cccaaatcaa 1630

<210> 422  
<211> 394  
<212> PRT  
<213> Homo sapiens

<400> 422  
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Tyr Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu  
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Thr Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln  
35 40 45  
Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser  
50 55 60  
Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser  
65 70 75  
Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu  
80 85 90  
Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp  
95 100 105  
Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg Leu  
110 115 120  
Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val  
125 130 135  
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu  
140 145 150  
Ile Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val

155					160					165				
Thr	Lys	Val	Glu	Trp	Ile	Phe	Ser	Gly	Arg	Arg	Ala	Lys	Glu	Glu
				170					175					180
Ile	Val	Phe	Arg	Tyr	Tyr	His	Lys	Leu	Arg	Met	Ser	Val	Glu	Tyr
				185					190					195
Ser	Gln	Ser	Trp	Gly	His	Phe	Gln	Asn	Arg	Val	Asn	Leu	Val	Gly
				200					205					210
Asp	Ile	Phe	Arg	Asn	Asp	Gly	Ser	Ile	Met	Leu	Gln	Gly	Val	Arg
				215					220					225
Glu	Ser	Asp	Gly	Gly	Asn	Tyr	Thr	Cys	Ser	Ile	His	Leu	Gly	Asn
				230					235					240
Leu	Val	Phe	Lys	Lys	Thr	Ile	Val	Leu	His	Val	Ser	Pro	Glu	Glu
				245					250					255
Pro	Arg	Thr	Leu	Val	Thr	Pro	Ala	Ala	Leu	Arg	Pro	Leu	Val	Leu
				260					265					270
Gly	Gly	Asn	Gln	Leu	Val	Ile	Ile	Val	Gly	Ile	Val	Cys	Ala	Thr
				275					280					285
Ile	Leu	Leu	Leu	Pro	Val	Leu	Ile	Leu	Ile	Val	Lys	Lys	Thr	Cys
				290					295					300
Gly	Asn	Lys	Ser	Ser	Val	Asn	Ser	Thr	Val	Leu	Val	Lys	Asn	Thr
				305					310					315
Lys	Lys	Thr	Asn	Pro	Glu	Ile	Lys	Glu	Lys	Pro	Cys	His	Phe	Glu
				320					325					330
Arg	Cys	Glu	Gly	Glu	Lys	His	Ile	Tyr	Ser	Pro	Ile	Ile	Val	Arg
				335					340					345
Glu	Val	Ile	Glu	Glu	Glu	Glu	Pro	Ser	Glu	Lys	Ser	Glu	Ala	Thr
				350					355					360
Tyr	Met	Thr	Met	His	Pro	Val	Trp	Pro	Ser	Leu	Arg	Ser	Asp	Arg
				365					370					375
Asn	Asn	Ser	Leu	Glu	Lys	Lys	Ser	Gly	Gly	Gly	Met	Pro	Lys	Thr
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Gln Gln Ala Phe

<210> 423  
 <211> 963  
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 ccattctcaca tgggttctacc ctactaaaga caggaagatc ataaactgac 100  
 agatactgaa attgtaagag ttggaaacta cattttgcaa agtcattgaa 150  
 ctctgagctc agttgcagta ctcgggaagc catgcaggat gaagatggat 200

acatcacctt aaatattaaa actcggaac cagctctcgt ctccgttggc 250  
 cctgcatacct cctcctggtg gcgtgtgatg gctttgattc tgctgatacct 300  
 gtgcgtgggg atggttgtcg ggctggtggc tctggggatt tggctctgtca 350  
 tgcagcgcaa ttacctacaa gatgagaatg aaaatcgcac aggaactctg 400  
 caacaattag caaagcgctt ctgtcaatat gtggtaaaac aatcagaact 450  
 aaagggcact ttcaaaggct ataaatgcag cccctgtgac acaaactgga 500  
 gatattatgg agatagctgc tatgggttct tcaggcacaa cttacatgg 550  
 gaagagagta agcagtactg cactgacatg aatgctactc tcctgaagat 600  
 tgacaaccgg aacattgtgg agtacatcaa agccaggact catttaattc 650  
 gttgggtcgg attatctcgc cagaagtcga atgaggtctg gaagtgggag 700  
 gatggctcgg ttatctcaga aaatatgttt gagtttttgg aagatggaaa 750  
 aggaaatatg aattgtgctt attttcataa tgggaaaatg caccctacct 800  
 tctgtgagaa caaacattat ttaatgtgtg agaggaaggc tggcatgacc 850  
 aaggtggacc aactacctta atgcaaagag gtggacagga taacacagat 900  
 aagggtctta ttgtacaata aaagatatgt atgaatgcat cagtagctga 950  
 aaaaaaaaaa aaa 963

<210> 424  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 424  
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 1 5 10 15  
 Lys Pro Ala Leu Val Ser Val Gly Pro Ala Ser Ser Ser Trp Trp  
 20 25 30  
 Arg Val Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val  
 35 40 45  
 Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn  
 50 55 60  
 Tyr Leu Gln Asp Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln  
 65 70 75  
 Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser Glu Leu  
 80 85 90  
 Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr Asn  
 95 100 105  
 Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn  
 110 115 120  
 Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp Met Asn Ala

	125		130		135
Thr Leu Leu Lys	Ile Asp Asn Arg Asn	Ile Val Glu Tyr Ile	Lys		
	140	145	150		
Ala Arg Thr His	Leu Ile Arg Trp Val	Gly Leu Ser Arg Gln	Lys		
	155	160	165		
Ser Asn Glu Val	Trp Lys Trp Glu Asp	Gly Ser Val Ile Ser	Glu		
	170	175	180		
Asn Met Phe Glu	Phe Leu Glu Asp Gly	Lys Gly Asn Met Asn	Cys		
	185	190	195		
Ala Tyr Phe His	Asn Gly Lys Met His	Pro Thr Phe Cys Glu	Asn		
	200	205	210		
Lys His Tyr Leu	Met Cys Glu Arg Lys	Ala Gly Met Thr Lys	Val		
	215	220	225		

Asp Gln Leu Pro

<210> 425  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 425  
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<210> 426  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 426  
 ctgagataac cgagccatcc tcccac 26

<210> 427  
 <211> 49  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 427  
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<210> 428  
 <211> 21  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 428  
ccaccaatgg cagccccacc t 21

<210> 429  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 429  
gactgccctc cctgcca 17

<210> 430  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 430  
caaaaagcct ggaagtcttc aaag 24

<210> 431  
<211> 20  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 431  
cagctggact gcaggtgcta 20

<210> 432  
<211> 22  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 432  
cagtgagcac agcaagtgtc ct 22

<210> 433  
<211> 28  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 433  
ggccacctcc ttgagtcttc agttccct 28

<210> 434  
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<220>  
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 <400> 434  
 caactactgg ctaaagctgg tgaa 24  
  
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 cctttctgta taggtgatac ccaatga 27  
  
 <210> 436  
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 <400> 436  
 tggccatccc taccagaggc aaaa 24  
  
 <210> 437  
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 <400> 437  
 ctgaagacga cgcggttac ta 22  
  
 <210> 438  
 <211> 19  
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 ggcagaaatg ggaggcaga 19  
  
 <210> 439  
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 <400> 439  
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 <210> 440  
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 <210> 441  
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 <210> 444  
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 cctggctcta gcaccaactc ata 23  
  
 <210> 445  
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 <400> 445  
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<210> 446  
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 <400> 448  
 tctttggcca tttcccatgg ctca 24  
  
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 cccatggcga ggaggaat 18  
  
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 tgcgtacgtg tgccttcag 19  
  
 <210> 451  
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<400> 451  
 cagcacccca ggcagtctgt gtgt 24  
  
 <210> 452  
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 <400> 452  
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 <210> 453  
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 cacagcatat tcagatgact aaatcca 27  
  
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 <400> 454  
 ttgttttagtt ctccaccgtg tctccacaga a 31  
  
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 <211> 21  
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 <400> 455  
 tgtcagaatg caacctggct t 21  
  
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 <210> 459  
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 <400> 459  
 ctccctgtacg gtctgctcac ttat 24  
  
 <210> 460  
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 tggctgtcag tccagtgtgc atgg 24  
  
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 <400> 462  
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<212> DNA  
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<220>  
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<400> 463  
aagttgctaa atatatacat tatctgcgcc aagtcca 37

<210> 464  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 464  
gtgctgcca caattcatga 20

<210> 465  
<211> 26  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 465  
gtccttggtgta tgggtctgaa ttatat 26

<210> 466  
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<220>  
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<400> 466  
actctctgca cccacagtc accactatct c 31

<210> 467  
<211> 22  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 467  
ctgaggaacc agccatgtct ct 22

<210> 468  
<211> 23  
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<220>  
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<400> 468  
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<210> 469  
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 ggggtggaggc tcaactgagta ga 22  
  
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 ccgtcgttca gcaacatgac 20  
  
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 cccaacttct cccttttgga ccct 24  
  
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 gtcccttcac tgtttagagc atga 24  
  
 <210> 483  
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 <400> 483  
 actctcccc tcaacagcct cctgag 26  
  
 <210> 484  
 <211> 20  
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 <400> 484  
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 <210> 485  
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 <212> DNA  
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 <400> 485  
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 <210> 486  
 <211> 21

<212> DNA  
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<220>  
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<400> 486  
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<210> 487  
<211> 23  
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<213> Artificial Sequence

<220>  
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<400> 487  
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<210> 488  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 488  
atagagggct cccagaagtg 20

<210> 489  
<211> 21  
<212> DNA  
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<220>  
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<400> 489  
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<210> 490  
<211> 19  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 490  
gctcagccaa acactgtca 19

<210> 491  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 491  
ggggccctga cagtgtt 17

<210> 492  
<211> 26  
<212> DNA  
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<220>  
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<400> 492  
ctgagccgag actggagcat ctacac 26

<210> 493  
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<212> DNA  
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<220>  
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<400> 493  
gtgggcagcg tcttgctc 17

<210> 494  
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cagcccgcgc gggagccgga ccgccgccgg aggagctcgg acggcatgct 150  
gagccccctc ctttgctgaa gcccgagtgc ggagaagccc gggcaaacgc 200  
aggctaagga gaccaaagcg gcgaagtgcg gagacagcgg acaagcagcg 250  
gaggagaagg aggaggaggc gaaccagag aggggcagca aaagaagcgg 300  
tggtggtggg cgtcgtggcc atggcgccgg ctatcgccag ctcgctcctc 350  
cgtcagaaga ggcaagcccg cgagcgcgag aaatccaacg cctgcaagtg 400  
tgtcagcagc ccagcaaag gcaagaccag ctgcgacaaa aacaagttaa 450  
atgtcttttc ccgggtcaaa ctcttcggct ccaagaagag gcgcagaaga 500  
agaccagagc ctgagcttaa gggatatagt accaagctat acagccgaca 550  
aggctaccac ttgcagctgc aggcggatgg aaccattgat ggcaccaaag 600  
atgaggacag cacttacact ctgtttaacc tcatccctgt gggctctgcga 650  
gtggtggcta tccaaggagt tcaaaccaag ctgtacttgg caatgaacag 700  
tgagggatac ttgtacacct cggaactttt cacacctgag tgcaaattca 750  
aagaatcagt gtttgaaaat tattatgtga catattcctc aatgatatac 800  
cgtcagcagc agtcaggccg aggggtggtat ctgggtctga acaaagaagg 850  
agagatcatg aaaggcaacc atgtgaagaa gaacaagcct gcagctcatt 900

ttctgcctaa accactgaaa gtggccatgt acaaggagcc atcactgcac 950  
 gatctcacgg agttctcccg atctggaagc gggaccccaa ccaagagcag 1000  
 aagtgtctct ggcgtgctga acggaggcaa atccatgagc cacaatgaat 1050  
 caacgtagcc agtgagggca aaagaagggc tctgtaacag aaccttacct 1100  
 ccagggtgctg ttgaattctt ctagcagtcc ttcacccaaa agttcaaatt 1150  
 tgtcagtgcac atttaccaaaa caaacaggca gaggttcacta ttctatctgc 1200  
 cattagacct tcttatcatc cataactaaag c 1231

<210> 495  
 <211> 245  
 <212> PRT  
 <213> Homo Sapien

<400> 495  
 Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln 15  
 1 5 10  
 Ala Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser 30  
 20 25 30  
 Pro Ser Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val 45  
 35 40 45  
 Phe Ser Arg Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg 60  
 50 55 60  
 Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser 75  
 65 70 75  
 Arg Gln Gly Tyr His Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp 90  
 80 85 90  
 Gly Thr Lys Asp Glu Asp Ser Thr Tyr Thr Leu Phe Asn Leu Ile 105  
 95 100 105  
 Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Gln Thr Lys 120  
 110 115 120  
 Leu Tyr Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr Ser Glu 135  
 125 130 135  
 Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu Asn 150  
 140 145 150  
 Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr Arg Gln Gln Gln Ser 165  
 155 160 165  
 Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu Gly Glu Ile Met 180  
 170 175 180  
 Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala His Phe Leu 195  
 185 190 195  
 Pro Lys Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser Leu His 210  
 200 205 210  
 Asp Leu Thr Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr Lys

	215		220		225
Ser Arg Ser Val	Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser				
	230		235		240
His Asn Glu Ser Thr					
	245				

<210> 496  
 <211> 1471  
 <212> DNA  
 <213> Homo Sapien

<400> 496  
 ccaggatgga gctggggcct gtatagccat attattgttc tatgctacta 50  
 gacatggggg ggacttggtg aaaaaggtat tatccagcca gagggctctgg 100  
 gagccctgtc ttactgaacc tgggcaacct ggatattctg agacatattt 150  
 tgggggggatt tcagtgaaaa aagtggggga tcccctccat ttagagtgtg 200  
 gcaaaggaaa aaacaccaag gttgggttcc ttctgacat tggcagtgcc 250  
 ccagtagggg tgggatgagc gaatattccc aaagctaaag tcccacaccc 300  
 tgtagattac aagagtggat ttggcaggag tgtgccccaa aatacagtgg 350  
 aaaggtgcct gaagatattt aaaccacgtc ttggaaattt agtgggtctt 400  
 ggcttttggg taggtgaagt gaggacagac actggagagg agggaaaggg 450  
 gacgttttca ataggaggca aaactcgagg gtgggatcca ctgaggagta 500  
 cataggctgc tggatctggt ggagccagca ctgggcccac ggggtggtaac 550  
 tggctgctgt ggaggggggt acgtgagggg ggggtctggg gcttatactc 600  
 aggtcctgtg ggtggggcag cgagtcgggg cctgagcgtc aagagcatgc 650  
 cctagtgagc gggctcctct gggggagccc agcgcgctcc gggcgctgc 700  
 cggttttggg gtgtctctc cggggcgct atggcggcgc tggccagtag 750  
 cctgatccgg cagaagcggg aggtccgcga gcccgggggc agccggccgg 800  
 tgtcggcgca gcggcgctg tgtccccgcg gcaccaagtc cctttgccag 850  
 aagcagctcc tcctcctgt gtccaagggt cgactgtgcg gggggcggcc 900  
 cgcgcgccg gaccgcggcc cgagacctca gctcaaaggc atcgtcacca 950  
 aactgttctg ccgccagggt ttctacctcc aggcgaatcc cgacggaagc 1000  
 atccagggca cccagagga taccagctcc ttacccact tcaacctgat 1050  
 ccctgtgggc ctccgtgtgg tcaccatcca gagcgccaag ctgggtcact 1100  
 acatggccat gaatgctgag ggactgctct acagttcgcc gcatttcaca 1150  
 gctgagtgtc gctttaagga gtgtgtcttt gagaattact acgtcctgta 1200  
 cgctctgtct ctctaccgcc agcgtcgttc tggcggggcc tggtaacctg 1250

gcctggacaa ggagggccag gtcatgaagg gaaaccgagt taagaagacc 1300  
aaggcagctg cccactttct gcccaagctc ctggaggtgg ccatgtacca 1350  
ggagccttct ctccacagtg tccccgaggc ctccccctcc agtccccctg 1400  
ccccctgaaa tgtagtccct ggactggagg ttccctgcac tcccagtgag 1450  
ccagccacca ccacaacctg t 1471

<210> 497  
<211> 225  
<212> PRT  
<213> Homo Sapien

<400> 497  
Met Ala Ala Leu Ala Ser Ser Leu Ile Arg Gln Lys Arg Glu Val  
1 5 10 15  
Arg Glu Pro Gly Gly Ser Arg Pro Val Ser Ala Gln Arg Arg Val  
20 25 30  
Cys Pro Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile  
35 40 45  
Leu Leu Ser Lys Val Arg Leu Cys Gly Gly Arg Pro Ala Arg Pro  
50 55 60  
Asp Arg Gly Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu  
65 70 75  
Phe Cys Arg Gln Gly Phe Tyr Leu Gln Ala Asn Pro Asp Gly Ser  
80 85 90  
Ile Gln Gly Thr Pro Glu Asp Thr Ser Ser Phe Thr His Phe Asn  
95 100 105  
Leu Ile Pro Val Gly Leu Arg Val Val Thr Ile Gln Ser Ala Lys  
110 115 120  
Leu Gly His Tyr Met Ala Met Asn Ala Glu Gly Leu Leu Tyr Ser  
125 130 135  
Ser Pro His Phe Thr Ala Glu Cys Arg Phe Lys Glu Cys Val Phe  
140 145 150  
Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala Leu Tyr Arg Gln Arg  
155 160 165  
Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp Lys Glu Gly Gln  
170 175 180  
Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Ala Ala Ala His  
185 190 195  
Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu Pro Ser  
200 205 210  
Leu His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala Pro  
215 220 225

<210> 498  
<211> 744

<212> DNA  
<213> Homo Sapien

<400> 498  
atggcgcgcg ccacgcctag cggcttgatc cgccagaagc ggcaggcgcg 50  
ggagcagcac tgggaccggc cgtctgccag caggaggcgg agcagcccca 100  
gcaagaaccg cgggctctgc aacggcaacc tggatgatat cttctccaaa 150  
gtgcgcctct tcggcctcaa gaagcgagg ttgcggcgcc aagatcccca 200  
gctcaagggg atagtgaaca ggttatattg caggcaaggc tactacttgc 250  
aaatgcaccc cgatggagct ctcgatggaa ccaaggatga cagcactaat 300  
tctacactct tcaacctcat accagtggga ctacgtgttg ttgccatcca 350  
gggagtgaac acaggggttg atatagccat gaatggagaa gggtacctct 400  
acctatcaga actttttacc cctgaatgca agtttaaaga atctgttttt 450  
gaaaattatt atgtaatcta ctcatccatg ttgtacagac aacaggaatc 500  
tggtagagcc tggtttttgg gattaaataa ggaagggcaa gctatgaaag 550  
ggaacagagt aaagaaaacc aaaccagcag ctcattttct acctaaagca 600  
ttggaagttg ccatgtaccg agaaccatct ttgcatgatg ttggggaaac 650  
ggccccgaag cctgggggtga cgccaagtaa aagcacaagt gcgtctgcaa 700  
taatgaatgg aggcaaacca gtcaacaaga gtaagacaac atag 744

<210> 499  
<211> 247  
<212> PRT  
<213> Homo Sapien

<400> 499  
Met Ala Ala Ala Ile Ala Ser Gly Leu Ile Arg Gln Lys Arg Gln  
1 5 10 15  
Ala Arg Glu Gln His Trp, Asp Arg Pro Ser Ala Ser Arg Arg Arg  
20 25 30  
Ser Ser Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val  
35 40 45  
Asp Ile Phe Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg  
50 55 60  
Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu  
65 70 75  
Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala  
80 85 90  
Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn  
95 100 105  
Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys  
110 115 120

Thr Gly Leu Tyr	Ile Ala Met Asn Gly	Glu Gly Tyr Leu Tyr Pro
	125	130 135
Ser Glu Leu Phe	Thr Pro Glu Cys Lys	Phe Lys Glu Ser Val Phe
	140	145 150
Glu Asn Tyr Tyr	Val Ile Tyr Ser Ser	Met Leu Tyr Arg Gln Gln
	155	160 165
Glu Ser Gly Arg	Ala Trp Phe Leu Gly	Leu Asn Lys Glu Gly Gln
	170	175 180
Ala Met Lys Gly	Asn Arg Val Lys Lys	Thr Lys Pro Ala Ala His
	185	190 195
Phe Leu Pro Lys	Pro Leu Glu Val Ala	Met Tyr Arg Glu Pro Ser
	200	205 210
Leu His Asp Val	Gly Glu Thr Val Pro	Lys Pro Gly Val Thr Pro
	215	220 225
Ser Lys Ser Thr	Ser Ala Ser Ala Ile	Met Asn Gly Gly Lys Pro
	230	235 240
Val Asn Lys Ser	Lys Thr Thr	
	245	

<210> 500  
 <211> 2906  
 <212> DNA  
 <213> Homo Sapien

<400> 500  
 ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50  
 ggctgttggg tgccttgcaa aatgaagga tgcaggacgc agctttctcc 100  
 tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150  
 gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200  
 acacaggagg cattcaagaa tgaaataaac cagagttaga cccgcggggg 250  
 ttggtgtggt ctgacataaa taaataatct taaagcagct gttcccctcc 300  
 ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcaca 350  
 agaaaaaagt atgttcattt ttctctataa aggagaaaagt gagccaagga 400  
 gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450  
 ggtgtggtgg tgttttcctt tctttttgaa tttcccacaa gaggagagga 500  
 aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550  
 gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600  
 tttgtgcta tgttgactaa aattgacgga taattgcagt tggatttttc 650  
 ttcatacaacc tccttttttt taaattttta ttccttttgg tatcaagatc 700  
 atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800  
 ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850  
 ataggtccta gggttaacag ggccctatTTT gacccctgc ttgtggtgct 900  
 gctggctctt caacttcttg tggTggctgg tctggtgcgg gctcagacct 950  
 gcccttctgt gtgctcctgc agcaaccagt tcagcaaggT gatttTgtgtt 1000  
 cggaataacc tgctgtaggt tccggatggc atctccacca acacacggct 1050  
 gctgaacctc catgagaacc aaatccagat catcaaagtT aacagcttca 1100  
 agcacttgag gcacttgga atcctacagt tgagtaggaa ccatatcaga 1150  
 accattgaaa ttggggcttt caatggTctg gcgaacctca acactctgga 1200  
 actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250  
 tgtctaaact gaaggagctc tggTtgcgaa acaaccccat tgaaagcatc 1300  
 cttcttatg cttttaacag aattccttct ttgcgcgcac tagacttagg 1350  
 ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggTctgt 1400  
 ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450  
 aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500  
 tttatctgcc atcaggcctg gctctttcca gggTttgatg caccttcaaa 1550  
 aactgtggat gatacagtcc cagattcaag tgattgaaag gaatgccttt 1600  
 gacaaccttc agtcaactagt ggagatcaac ctggcacaca ataatctaac 1650  
 attactgcct catgacctct tcactccctt gcatcatcta gagcggatac 1700  
 atttacatca caacccttg aactgtaaact gtgacatact gtggctcagc 1750  
 tggTggataa aagacatggc cccctcgaac acagcttgTt gtgcccggTg 1800  
 taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850  
 attacttcac atgctatgct ccggTgattg tggagcccc tgcagacctc 1900  
 aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950  
 cctgacatct gtatcttgga ttactccaaa tggaacagtc atgacacatg 2000  
 gggcgtacaa agtgcggata gctgtgctca gtgatggTac gttaaatttc 2050  
 acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggTgagtaa 2100  
 ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150  
 ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200  
 ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtccactcc 2250  
 agtggTcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300  
 gcacaaggTc gacagagaaa accttcacca tcccagTgac tgatataaac 2350

agtgggatcc caggaattga tgaggtcatg aagactacca aaatcatcat 2400  
 tgggtgtttt gtggccatca cactcatggc tgcaagtgatg ctggtcattt 2450  
 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500  
 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550  
 catggaaagc cacctgcccc tgccctgctat cgagcatgag cacctaaatc 2600  
 actataactc atacaaatct ccttcaacc acacaacaac agttaacaca 2650  
 ataaattcaa tacacagttc agtgcataaa ccgttattga tccgaatgaa 2700  
 ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750  
 caaaaaaaca acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaaca 2850  
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900  
 caaaaa 2906

<210> 501  
 <211> 640  
 <212> PRT  
 <213> Homo Sapien

<400> 501  
 Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly  
 1 5 10 15  
 Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu  
 20 25 30  
 Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln  
 35 40 45  
 Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val  
 50 55 60  
 Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser  
 65 70 75  
 Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile  
 80 85 90  
 Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu  
 95 100 105  
 Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe  
 110 115 120  
 Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg  
 125 130 135  
 Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu  
 140 145 150  
 Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser  
 155 160 165

Tyr	Ala	Phe	Asn	Arg	Ile	Pro	Ser	Leu	Arg	Arg	Leu	Asp	Leu	Gly	170	175	180
Glu	Leu	Lys	Arg	Leu	Ser	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	Glu	Gly	185	190	195
Leu	Ser	Asn	Leu	Arg	Tyr	Leu	Asn	Leu	Ala	Met	Cys	Asn	Leu	Arg	200	205	210
Glu	Ile	Pro	Asn	Leu	Thr	Pro	Leu	Ile	Lys	Leu	Asp	Glu	Leu	Asp	215	220	225
Leu	Ser	Gly	Asn	His	Leu	Ser	Ala	Ile	Arg	Pro	Gly	Ser	Phe	Gln	230	235	240
Gly	Leu	Met	His	Leu	Gln	Lys	Leu	Trp	Met	Ile	Gln	Ser	Gln	Ile	245	250	255
Gln	Val	Ile	Glu	Arg	Asn	Ala	Phe	Asp	Asn	Leu	Gln	Ser	Leu	Val	260	265	270
Glu	Ile	Asn	Leu	Ala	His	Asn	Asn	Leu	Thr	Leu	Leu	Pro	His	Asp	275	280	285
Leu	Phe	Thr	Pro	Leu	His	His	Leu	Glu	Arg	Ile	His	Leu	His	His	290	295	300
Asn	Pro	Trp	Asn	Cys	Asn	Cys	Asp	Ile	Leu	Trp	Leu	Ser	Trp	Trp	305	310	315
Ile	Lys	Asp	Met	Ala	Pro	Ser	Asn	Thr	Ala	Cys	Cys	Ala	Arg	Cys	320	325	330
Asn	Thr	Pro	Pro	Asn	Leu	Lys	Gly	Arg	Tyr	Ile	Gly	Glu	Leu	Asp	335	340	345
Gln	Asn	Tyr	Phe	Thr	Cys	Tyr	Ala	Pro	Val	Ile	Val	Glu	Pro	Pro	350	355	360
Ala	Asp	Leu	Asn	Val	Thr	Glu	Gly	Met	Ala	Ala	Glu	Leu	Lys	Cys	365	370	375
Arg	Ala	Ser	Thr	Ser	Leu	Thr	Ser	Val	Ser	Trp	Ile	Thr	Pro	Asn	380	385	390
Gly	Thr	Val	Met	Thr	His	Gly	Ala	Tyr	Lys	Val	Arg	Ile	Ala	Val	395	400	405
Leu	Ser	Asp	Gly	Thr	Leu	Asn	Phe	Thr	Asn	Val	Thr	Val	Gln	Asp	410	415	420
Thr	Gly	Met	Tyr	Thr	Cys	Met	Val	Ser	Asn	Ser	Val	Gly	Asn	Thr	425	430	435
Thr	Ala	Ser	Ala	Thr	Leu	Asn	Val	Thr	Ala	Ala	Thr	Thr	Thr	Pro	440	445	450
Phe	Ser	Tyr	Phe	Ser	Thr	Val	Thr	Val	Glu	Thr	Met	Glu	Pro	Ser	455	460	465
Gln	Asp	Glu	Ala	Arg	Thr	Thr	Asp	Asn	Asn	Val	Gly	Pro	Thr	Pro	470	475	480

Val	Val	Asp	Trp	Glu	Thr	Thr	Asn	Val	Thr	Thr	Ser	Leu	Thr	Pro	485	490	495
Gln	Ser	Thr	Arg	Ser	Thr	Glu	Lys	Thr	Phe	Thr	Ile	Pro	Val	Thr	500	505	510
Asp	Ile	Asn	Ser	Gly	Ile	Pro	Gly	Ile	Asp	Glu	Val	Met	Lys	Thr	515	520	525
Thr	Lys	Ile	Ile	Ile	Gly	Cys	Phe	Val	Ala	Ile	Thr	Leu	Met	Ala	530	535	540
Ala	Val	Met	Leu	Val	Ile	Phe	Tyr	Lys	Met	Arg	Lys	Gln	His	His	545	550	555
Arg	Gln	Asn	His	His	Ala	Pro	Thr	Arg	Thr	Val	Glu	Ile	Ile	Asn	560	565	570
Val	Asp	Asp	Glu	Ile	Thr	Gly	Asp	Thr	Pro	Met	Glu	Ser	His	Leu	575	580	585
Pro	Met	Pro	Ala	Ile	Glu	His	Glu	His	Leu	Asn	His	Tyr	Asn	Ser	590	595	600
Tyr	Lys	Ser	Pro	Phe	Asn	His	Thr	Thr	Thr	Val	Asn	Thr	Ile	Asn	605	610	615
Ser	Ile	His	Ser	Ser	Val	His	Glu	Pro	Leu	Leu	Ile	Arg	Met	Asn	620	625	630
Ser	Lys	Asp	Asn	Val	Gln	Glu	Thr	Gln	Ile						635	640	

<210> 502  
 <211> 2458  
 <212> DNA  
 <213> Homo Sapien

<400> 502  
 gcgccgggag cccatctgcc ccaggggca cggggcgcg ggccgggtcc 50  
 cgcccgccac atggctgcag ccacctcgcg cgcaccccg ggcgcgcgc 100  
 ccagctcgcc cgaggtccgt cggaggcgcc cggccgccc ggagccaagc 150  
 agcaactgag cggggaagcg ccgcgctccg gggatcgga tgtccctcct 200  
 ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250  
 ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300  
 caactggggc ttccagaaaa agacactctg gatattgaat ggctgtcac 350  
 cgataatgaa gggaaccaa aagtggatgat cacttactcc agtcgtcatg 400  
 tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450  
 aatttcctgg caggagatgc ctcttgacag attgaacctc tgaagcccag 500  
 tgatgagggc cggtaacact gtaagggtta gaattcagg cgctacgtgt 550  
 ggagccatgt catcttaaaa gtcttagtga gaccatcaa gcccaagtgt 600

gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650  
gtcatcctct ggcacagagc ccattgtgta ttactggcag cgaatccgag 700  
agaaagaggg agaggatgaa cgtctgcctc ccaaactctag gattgactac 750  
aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800  
actgtaccag tgcacagcag gcaacgaagc tgggaaggaa agctgtgtgg 850  
tgcgagtaac tgtacagtat gtacaaagca tcggcatggt tgcaggagca 900  
gtgacaggca tagtggctgg agccctgctg attttctct tgggtgtggct 950  
gctaataccg aggaaagaca aagaaagata tgaggaagaa gagagacct 1000  
atgaaattcg agaagatgct gaagctccaa aagcccgtct tgtgaaacct 1050  
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tcgctccaca gcaaatagtg cctcacgcag ccagcggaca ctgtcaactg 1150  
acgcagcacc ccagccaggg ctggccaccc aggcatacag cctagtgggg 1200  
ccagagggtga gaggttctga accaaagaaa gtccaccatg ctaatctgac 1250  
caaagcagaa accacacca gcatgatccc cagccagagc agagccttcc 1300  
aaacggtctg aattacaatg gacttgactc ccacgcttcc ctaggagtca 1350  
gggtctttgg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400  
ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450  
aga'tgagcat tttccttata caataccaaa caagcaaaag gatgtaagct 1500  
gattcatctg taaaaaggca tcttattgtg ccttttagacc agagtaaggg 1550  
aaagcaggag tccaaatcta tttgttgacc aggacctgtg gtgagaagg 1600  
tggggaaagg tgaggatgaat atacctaaaa cttttaatgt gggatatttt 1650  
gtatcagtgc tttgattcac aattttcaag aggaaatggg atgctgtttg 1700  
taaatcttct atgcatttct gcaaacttat tggattatta gttattcaga 1750  
cagtcaagca gaaccacag ccttattaca cctgtctaca ccatgtactg 1800  
agctaaccac ttctaagaaa ctccaaaaaa ggaaacatgt gtcttctatt 1850  
ctgacttaac ttcatctgtc ataagggttg gatattaatt tcaaggggag 1900  
ttgaaatagt gggagatgga gaagagtga tgagtttctc ccaactctata 1950  
ctaactctac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000  
aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050  
ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100  
cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150  
agaaaataca acatgtcatt tatcaacgct cttagaaaga attcttctag 2200

agaaaaaggg atctaggaat gctgaaagat tacccaacat accattatag 2250  
tctcttcttt ctgagaaaaat gtgaaaccag aattgcaaga ctgggtggac 2300  
tagaaagggg gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350  
cgggcatggt gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400  
gtgagccgag attatgccat tgcactccag cctgggtgac agagcgggac 2450  
tccgtctc 2458

<210> 503  
<211> 373  
<212> PRT  
<213> Homo Sapien

<400> 503  
Met Ser Leu Leu Leu Leu Leu Leu Val Ser Tyr Tyr Val Gly  
1 5 10 15  
Thr Leu Gly Thr His Thr Glu Ile Lys Arg Val Ala Glu Glu Lys  
20 25 30  
Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp  
35 40 45  
Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln  
50 55 60  
Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu  
65 70 75  
Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu  
80 85 90  
Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp  
95 100 105  
Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val  
110 115 120  
Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro  
125 130 135  
Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr  
140 145 150  
Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr  
155 160 165  
Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro  
170 175 180  
Pro Lys Ser Arg Ile Asp Tyr Asn His Pro Gly Arg Val Leu Leu  
185 190 195  
Gln Asn Leu Thr Met Ser Tyr Ser Gly Leu Tyr Gln Cys Thr Ala  
200 205 210  
Gly Asn Glu Ala Gly Lys Glu Ser Cys Val Val Arg Val Thr Val  
215 220 225

Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly	230	235	240
Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu	245	250	255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Glu Arg Pro	260	265	270
Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val	275	280	285
Lys Pro Ser Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly	290	295	300
Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln	305	310	315
Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr	320	325	330
Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro	335	340	345
Lys Lys Val His His Ala Asn Leu Thr Lys Ala Glu Thr Thr Pro	350	355	360
Ser Met Ile Pro Ser Gln Ser Arg Ala Phe Gln Thr Val	365	370	

<210> 504  
 <211> 3060  
 <212> DNA  
 <213> Homo Sapien

<400> 504  
 cgcgaggcgc ggggagcctg ggaccaggag cgagagccgc ctacctgcag 50  
 ccgccgccca cggcacggca gccaccatgg cgctcctgct gtgcttctgtg 100  
 ctctgtgtcg gtagtagtga tttcgccaga agtttgagta tcactactcc 150  
 tgaagagatg attgaaaaag ccaaagggga aactgcctat ctgccatgca 200  
 aatttacgct tagtcccga gaccagggac cgctggacat cgagtggctg 250  
 atatcaccag ctgataatca gaaggtggat caagtgatta ttttatattc 300  
 tggagacaaa atttatgatg actactatcc agatctgaaa ggccgagtac 350  
 attttacgag taatgatctc aaatctggtg atgcatcaat aaatgtaaog 400  
 aatttacaac tgtcagatat tggcacatat cagtgc aaag tgaaaaaagc 450  
 tctgtgtgtt gcaaataaga agattcatct ggtagttctt gttaagcctt 500  
 cagggtgcgag atgttacgtt gatggatctg aagaaattgg aagtgaacttt 550  
 aagataaaat gtgaaccaa aagaaggttca cttccattac agtatgagtg 600  
 gcaaaaattg tctgactcac agaaaatgcc cacttcatgg ttagcagaaa 650  
 tgacttcate tgttatatct gtaaaaaatg cctctttctga gtactctggg 700

acatacagct gtacagtcag aaacagagtg ggctctgac agtgccctgtt 750  
 gcgtctaaac gttgtccctc cttcaaataa agctggacta attgcaggag 800  
 ccattatagg aacttttgctt gctctagcgc tcattgggtct tatcatcttt 850  
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 gaagctacat cggcagtaat cattcatccc tgggggtccat gtctccttcc 1000  
 aacatggaag gatattccaa gactcagtat aaccaagtac caagtgaaga 1050  
 ctttgaacgc actcctcaga gtccgactct cccacctgct aagttcaagt 1100  
 acccttaciaa gactgatgga attacagttg tataaatatg gactactgaa 1150  
 gaatctgaag tattgtatta tttgacttta ttttaggcct ctagtaaaga 1200  
 cttaaagtgt ttttaaaaaa agcacaaggc acagagatta gagcagctgt 1250  
 aagaacacat ctactttatg caatggcatt agacatgtaa gtcagatgtc 1300  
 atgtcaaaat tagtacgagc caaattcttt gttaaaaaac cctatgtata 1350  
 gtgacactga tagttaaag atgttttatt atattttcaa taactaccac 1400  
 taacaaatth ttaacttttc atatgcatat tctgatatgt ggtcttttag 1450  
 gaaaagtatg gttaatagtt gatttttcaa aggaaattht aaaattctta 1500  
 cgttctgtth aatgtttttg ctatttagtt aaatacattg aagggaata 1550  
 cccgttctth tcccctthta tgcacacaac agaaacacgc gttgtcatgc 1600  
 ctcaaactat tttttatttg caactacatg atttcacaca attctcttaa 1650  
 acaacgacat aaaatagatt tccttgata taaataactt acatacgctc 1700  
 cataaagtaa attctcaaag gtgctagaac aaatcgcca cttctacagt 1750  
 gttctcgat ccaacagagt tgatgcacaa tatataaata ctcaagtcca 1800  
 atattaaaaa cttaggcact tgactaaactt taataaaatt tctcaacta 1850  
 tatcaatatc taaagtgcatt atatttttht agaaagatta ttctcaataa 1900  
 cttctataaa aataagtttg atggtttggc ccatctaact tcaactactat 1950  
 tagtaagaac ttttaactth taatgtgtag taaggtttat tctaccttht 2000  
 tctcaacatg acaccaacac aatcaaaaac gaagttagtg aggtgctaac 2050  
 atgtgaggat taatccagt attccggtca caatgcattc caggaggagg 2100  
 taccatgtc actggaattg ggcgatatgg tttattthtt cttccctgat 2150  
 ttggataacc aaatggaaca ggaggaggat agtgattctg atggccattc 2200  
 cctcgataca ttctggctt ttttctgggc aaagggtgcc acattggaag 2250  
 aggtggaaat ataagttctg aaatctgtag ggaagagaac acattaagtt 2300

aattcaaagg aaaaaatcat catctatggt ccagatttct cattaagac 2350  
aaagttaccc acaacactga gatcacatct aagtgacact cctattgtca 2400  
ggtctaaata cattaataaac ctcatgtgta ataggcgtat aatgtataac 2450  
aggtgaccaa tgttttctga atgcataaag aaatgaataa actcaaacac 2500  
agtacttcct aaacaacttc aaccaaaaaa gaccaaaaaca tggaacgaat 2550  
ggaagcttgt aaggacatgc ttgttttagt ccagtgggtt ccacagctgg 2600  
ctaagccagg agtcacttgg aggcctttta atacaaaaca ttggagctgg 2650  
aggccattat ccttagcaaa ctaatgcaga aacagaaaat caactaccgc 2700  
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gaaggaaaca atagacattg gagtctattt gagaggggag ggtgggagaa 2800  
ggaaaaggag cagaaaagat aactattgag tactgccttc acacctgggt 2850  
gatgaaataa tatgtacaac aaatccctgt gacacatgtt tacctatgga 2900  
acaaaccttc atgtgtatcc ctaaacctaa aataaaagt aaataaaaaa 2950  
aaataaaaaa aaataaaaaa aaataaaaaa aaataaaaaa aaataaaaaa 3000  
aaataaaaaa aaataaaaaa aaataaaaaa aaataaaaaa aaataaaaaa 3050  
aaataaaaaa 3060

<210> 505  
<211> 352  
<212> PRT  
<213> Homo Sapien

<400> 505  
Met Ala Leu Leu Leu Cys Phe Val Leu Leu Cys Gly Val Val Asp  
1 5 10 15  
Phe Ala Arg Ser Leu Ser Ile Thr Thr Pro Glu Glu Met Ile Glu  
20 25 30  
Lys Ala Lys Gly Glu Thr Ala Tyr Leu Pro Cys Lys Phe Thr Leu  
35 40 45  
Ser Pro Glu Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Ile Ser  
50 55 60  
Pro Ala Asp Asn Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser  
65 70 75  
Gly Asp Lys Ile Tyr Asp Asp Tyr Tyr Pro Asp Leu Lys Gly Arg  
80 85 90  
Val His Phe Thr Ser Asn Asp Leu Lys Ser Gly Asp Ala Ser Ile  
95 100 105  
Asn Val Thr Asn Leu Gln Leu Ser Asp Ile Gly Thr Tyr Gln Cys  
110 115 120  
Lys Val Lys Lys Ala Pro Gly Val Ala Asn Lys Lys Ile His Leu

	125	130	135
Val Val Leu Val	Lys 140	Pro Ser Gly Ala Arg Cys Tyr Val Asp Gly 145 150	
Ser Glu Glu Ile	Gly 155	Ser Asp Phe Lys Ile Lys Cys Glu Pro Lys 160 165	
Glu Gly Ser Leu	Pro 170	Leu Gln Tyr Glu Trp Gln Lys Leu Ser Asp 175 180	
Ser Gln Lys Met	Pro 185	Thr Ser Trp Leu Ala Glu Met Thr Ser Ser 190 195	
Val Ile Ser Val	Lys 200	Asn Ala Ser Ser Glu Tyr Ser Gly Thr Tyr 205 210	
Ser Cys Thr Val	Arg 215	Asn Arg Val Gly Ser Asp Gln Cys Leu Leu 220 225	
Arg Leu Asn Val	Val 230	Pro Pro Ser Asn Lys Ala Gly Leu Ile Ala 235 240	
Gly Ala Ile Ile	Gly 245	Thr Leu Leu Ala Leu Ala Leu Ile Gly Leu 250 255	
Ile Ile Phe Cys	Cys 260	Arg Lys Lys Arg Arg Glu Glu Lys Tyr Glu 265 270	
Lys Glu Val His	His 275	Asp Ile Arg Glu Asp Val Pro Pro Pro Lys 280 285	
Ser Arg Thr Ser	Thr 290	Ala Arg Ser Tyr Ile Gly Ser Asn His Ser 295 300	
Ser Leu Gly Ser	Met 305	Ser Pro Ser Asn Met Glu Gly Tyr Ser Lys 310 315	
Thr Gln Tyr Asn	Gln 320	Val Pro Ser Glu Asp Phe Glu Arg Thr Pro 325 330	
Gln Ser Pro Thr	Leu 335	Pro Pro Ala Lys Phe Lys Tyr Pro Tyr Lys 340 345	
Thr Asp Gly Ile	Thr 350	Val Val	

<210> 506  
 <211> 1705  
 <212> DNA  
 <213> Homo Sapien

<400> 506  
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 tctgattggt gaatggtgaa ggtgcctgtc taacttttct gtaaaaagaa 100  
 ccagctgcct ccaggcagcc agccctcaag catcacttac aggaccagag 150  
 ggacaagaca tgactgtgat gaggagctgc ttlogccaat ttaacaccaa 200  
 gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250

agatgaattt tcaacagagg ctgcaaagcc tgtggacttt agccagaccc 300  
 ttctgccctc ctttgctggc gacagcctct caaatgcaga tggttgtgct 350  
 cccttgccctg ggttttaccc tgcttctctg gagccaggta tcagggggccc 400  
 agggccaaga attccacttt gggccctgcc aagtgaaggg ggttggtccc 450  
 cagaaactgt gggaagcctt ctgggctgtg aaagacacta tgcaagctca 500  
 ggataacatc acgagtgcgc ggctgctgca gcaggagggt ctgcagaacg 550  
 tctcggatgc tgagagctgt taccttgtec acaccctgct ggagttctac 600  
 ttgaaaactg ttttcaaaaa ccaccacaat agaacagttg aagtcaggac 650  
 tctgaagtca ttctctactc tggccaacaa ctttggttctc atcgtgtcac 700  
 aactgcaacc cagtcaagaa aatgagatgt tttccatcag agacagtgca 750  
 cacaggcggg ttctgctatt ccggagagca ttcaaacagt tggacgtaga 800  
 agcagctctg accaaagccc ttgggggaagt ggacattctt ctgacctgga 850  
 tgcagaaatt ctacaagctc tgaatgtcta gaccaggacc tccctcccc 900  
 tggcactggg ttgttcctct tgtcatttca aacagtctcc ctctctatgc 950  
 tgttcaactg acacttcacg cccttgGCCa tgggtcccat tcttgGCCa 1000  
 ggattattgt caaagaagtc attctttaag cagcgccagt gacagtcagg 1050  
 gaaggTgcct ctggatgctg tgaagagtct acagagaaga ttcttgtatt 1100  
 tattacaact ctatttaatt aatgtcagta tttcaactga agttctattt 1150  
 atttgtgaga ctgtaagtta catgaaggca gcagaatatt gtgccccatg 1200  
 cttctttacc cctcacaatc cttgccacag tgtggggcag tggatgggtg 1250  
 cttagtaagt acttaataaa ctgtgggtgct ttttttggcc tgtctttgga 1300  
 ttgttaaaaa acagagaggg atgcttggtat gtaaaactga acttcagagc 1350  
 atgaaaaatca cactgtcttc tgatatctgc agggacagag cattgggggtg 1400  
 ggggtaaggt gcatctgttt gaaaagtaaa cgataaaatg tggattaaag 1450  
 tgcccagcac aaagcagatc ctcaataaac atttcatttc caccacacac 1500  
 tcgccagctc accccatcat ccccttccct tgggtgccctc cttttttttt 1550  
 tatcctagtc attcttccct aatcttccac ttgagtgtca agctgacctt 1600  
 gctgatgggt acattgcacc tggatgtact atccaatctg tgatgacatt 1650  
 ccctgctaatt aaaagacaac ataactccaa aaaaaaaaaa aaaaaaaaaa 1700  
 aaaaa 1705

<210> 507  
 <211> 206  
 <212> PRT

<213> Homo Sapien

<400> 507

Met	Asn	Phe	Gln	Gln	Arg	Leu	Gln	Ser	Leu	Trp	Thr	Leu	Ala	Arg	
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Pro	Phe	Cys	Pro	Pro	Leu	Leu	Ala	Thr	Ala	Ser	Gln	Met	Gln	Met	
				20					25					30	
Val	Val	Leu	Pro	Cys	Leu	Gly	Phe	Thr	Leu	Leu	Leu	Trp	Ser	Gln	
				35					40					45	
Val	Ser	Gly	Ala	Gln	Gly	Gln	Glu	Phe	His	Phe	Gly	Pro	Cys	Gln	
				50					55					60	
Val	Lys	Gly	Val	Val	Pro	Gln	Lys	Leu	Trp	Glu	Ala	Phe	Trp	Ala	
				65					70					75	
Val	Lys	Asp	Thr	Met	Gln	Ala	Gln	Asp	Asn	Ile	Thr	Ser	Ala	Arg	
				80					85					90	
Leu	Leu	Gln	Gln	Glu	Val	Leu	Gln	Asn	Val	Ser	Asp	Ala	Glu	Ser	
				95					100					105	
Cys	Tyr	Leu	Val	His	Thr	Leu	Leu	Glu	Phe	Tyr	Leu	Lys	Thr	Val	
				110					115					120	
Phe	Lys	Asn	His	His	Asn	Arg	Thr	Val	Glu	Val	Arg	Thr	Leu	Lys	
				125					130					135	
Ser	Phe	Ser	Thr	Leu	Ala	Asn	Asn	Phe	Val	Leu	Ile	Val	Ser	Gln	
				140					145					150	
Leu	Gln	Pro	Ser	Gln	Glu	Asn	Glu	Met	Phe	Ser	Ile	Arg	Asp	Ser	
				155					160					165	
Ala	His	Arg	Arg	Phe	Leu	Leu	Phe	Arg	Arg	Ala	Phe	Lys	Gln	Leu	
				170					175					180	
Asp	Val	Glu	Ala	Ala	Leu	Thr	Lys	Ala	Leu	Gly	Glu	Val	Asp	Ile	
				185					190					195	
Leu	Leu	Thr	Trp	Met	Gln	Lys	Phe	Tyr	Lys	Leu					
				200					205						

<210> 508

<211> 924

<212> DNA

<213> Homo Sapien

<400> 508

aaggagcagc ccgcaagcac caagtgagag gcatgaagtt acagtgtggt 50  
tccctttggc tcctgggtac aatactgata ttgtgctcag tagacaacca 100  
cggctctcagg agatgtctga tttccacaga catgcaccat atagaagaga 150  
gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaa 200  
gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250  
tgtgtgctgc gtgaccaaga acctcctggc gttctacgtg gacaggggtg 300

tcaaggatca tcaggagcca aacccccaaaa tcttgagaaa aatcagcagc 350  
attgccaaact ctttcctcta catgcagaaa actctgcggc aatgtcagga 400  
acagaggcag tgtcactgca ggcaggaagc caccaatgcc accagagtca 450  
tccatgacaa ctatgatcag ctggagggtcc acgctgctgc cattaatatcc 500  
ctgggagagc tcgacgtctt tctagcctgg attaataaga atcatgaagt 550  
aatgtttctca gcttgatgac aaggaacctg tatagtgatc cagggatgaa 600  
cacccccctgt gcggtttact gtgggagaca gccacacctg aaggggaagg 650  
agatggggaa ggccccttgc agctgaaagt cccactggct ggcctcaggc 700  
tgtcttattc cgcttgaaaa taggcaaaaa gtctactgtg gtatttgtaa 750  
taaactctat ctgctgaaag ggcctgcagg ccatcctggg agtaaagggc 800  
tgccttccca tctaatttat tgtaaagtca tatagtccat gtctgtgatg 850  
tgagccaagt gatatcctgt agtacacatt gtactgagtg gtttttctga 900  
ataaattcca tattttacct atga 924

<210> 509  
<211> 177  
<212> PRT  
<213> Homo Sapien

<400> 509  
Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu  
1 5 10 15  
Ile Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile  
20 25 30  
Ser Thr Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys  
35 40 45  
Arg Ala Ile Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu  
50 55 60  
Ser Thr Leu Glu Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys  
65 70 75  
Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg Val Phe  
80 85 90  
Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile Ser  
95 100 105  
Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln  
110 115 120  
Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn  
125 130 135  
Ala Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His  
140 145 150  
Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu Ala

155

160

165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala  
 170 175

&lt;210&gt; 510

&lt;211&gt; 996

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 510

cccgtgccaa gagtgacgta agtaccgcct atagagtcta taggcccact 50  
 tggcttcgtt agaacgoggc tacaattaat acataacctt atgtatcata 100  
 cacatacgat ttaggtgaca ctatagaata acatccactt tgcctttctc 150  
 tccacaggtg tccactccca ggtccaactg cacctcgggt ctatcgataa 200  
 tctcagcacc agccactcag agcagggcac gatgttgggg gcccgccctca 250  
 ggctctgggt ctgtgccttg tgcagcgtct gcagcatgag cgtcctcaga 300  
 gcctatccca atgcctcccc actgctcggc tccagctggg gtggcctgat 350  
 ccacctgtac acagccacag ccaggaacag ctaccacctg cagatccaca 400  
 agaatggcca tgtggatggc gcaccccatc agaccatcta cagtgccttg 450  
 atgatcagat cagaggatgc tggctttgtg gtgattacag gtgtgatgag 500  
 cagaagatac ctctgcatgg atttcagagg caacattttt ggatcacact 550  
 atttcgaccc ggagaactgc aggttccaac accagacgct ggaaaacggg 600  
 tacgacgtct accactctcc tcagtatcac ttcttgggtca gtctgggccg 650  
 ggccaagaga gccttcctgc caggcatgaa cccacccccg tactcccagt 700  
 tcctgtcccc gaggaacgag atccccctaa ttcaattcaa ccccccata 750  
 ccacggcggc acaccggag cgccgaggac gactcggagc gggaccccct 800  
 gaacgtgctg aagccccggg cccggatgac cccggccccg gcctcctggt 850  
 cacaggagct cccgagcgcc gaggacaaca gcccgatggc cagtgaacca 900  
 ttaggggttg tcagggcgcg tcgagtgaac acgcacgctg ggggaacggg 950  
 cccggaaggc tgccgcccct tcgccaagtt catctagggt cgctgg 996

&lt;210&gt; 511

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 511

Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser  
 1 5 10 15  
 Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro  
 20 25 30

Leu	Leu	Gly	Ser	Ser	Trp	Gly	Gly	Leu	Ile	His	Leu	Tyr	Thr	Ala	
				35					40					45	
Thr	Ala	Arg	Asn	Ser	Tyr	His	Leu	Gln	Ile	His	Lys	Asn	Gly	His	
				50					55					60	
Val	Asp	Gly	Ala	Pro	His	Gln	Thr	Ile	Tyr	Ser	Ala	Leu	Met	Ile	
				65					70					75	
Arg	Ser	Glu	Asp	Ala	Gly	Phe	Val	Val	Ile	Thr	Gly	Val	Met	Ser	
				80					85					90	
Arg	Arg	Tyr	Leu	Cys	Met	Asp	Phe	Arg	Gly	Asn	Ile	Phe	Gly	Ser	
				95					100					105	
His	Tyr	Phe	Asp	Pro	Glu	Asn	Cys	Arg	Phe	Gln	His	Gln	Thr	Leu	
				110					115					120	
Glu	Asn	Gly	Tyr	Asp	Val	Tyr	His	Ser	Pro	Gln	Tyr	His	Phe	Leu	
				125					130					135	
Val	Ser	Leu	Gly	Arg	Ala	Lys	Arg	Ala	Phe	Leu	Pro	Gly	Met	Asn	
				140					145					150	
Pro	Pro	Pro	Tyr	Ser	Gln	Phe	Leu	Ser	Arg	Arg	Asn	Glu	Ile	Pro	
				155					160					165	
Leu	Ile	His	Phe	Asn	Thr	Pro	Ile	Pro	Arg	Arg	His	Thr	Arg	Ser	
				170					175					180	
Ala	Glu	Asp	Asp	Ser	Glu	Arg	Asp	Pro	Leu	Asn	Val	Leu	Lys	Pro	
				185					190					195	
Arg	Ala	Arg	Met	Thr	Pro	Ala	Pro	Ala	Ser	Cys	Ser	Gln	Glu	Leu	
				200					205					210	
Pro	Ser	Ala	Glu	Asp	Asn	Ser	Pro	Met	Ala	Ser	Asp	Pro	Leu	Gly	
				215					220					225	
Val	Val	Arg	Gly	Gly	Arg	Val	Asn	Thr	His	Ala	Gly	Gly	Thr	Gly	
				230					235					240	
Pro	Glu	Gly	Cys	Arg	Pro	Phe	Ala	Lys	Phe	Ile					
				245					250						

<210> 512  
 <211> 2015  
 <212> DNA  
 <213> Homo Sapien

<400> 512  
 ggaaaaggta cccgcgagag acagccagca gttctgtgga gcagcgggtgg 50  
 ccggctagga tgggctgtct ctgggggtctg gctctgcccc ttttcttctt 100  
 ctgctgggag gttgggggtct ctgggagctc tgcaggcccc agcaccgcga 150  
 gagcagacac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200  
 ctagcaccgg gccacgccgc tctggaaact caaacgctga gcgctgagac 250  
 ctcttctagg gcctcaaccc cagccggccc cattccagaa gcagagacca 300

ggggagccaa gagaatttcc cctgcaagag agaccaggag tttcacaaaa 350  
 acatctccca acttcatggt gctgatcgcc acctcogtgg agacatcagc 400  
 cgccagtggc agccccgagg gagctggaat gaccacagtt cagaccatca 450  
 caggcagtga tcccaggagaa gccatctttg acaccctttg caccgatgac 500  
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 cacctccaca gaagctaagg gcctgtcctc agagagcagt gcctcttccg 600  
 acggccccca tccagtcac acccogtcac gggcctcaga gagcagcgcc 650  
 tcttccgacg gcccccatcc agtcacacc cgtcacggg cctcagagag 700  
 cagcgctct tccgacggcc cccatccagt catcaccccg tcatgggtccc 750  
 cgggatctga tgtcactctc ctgctgaag ccctgggtgac tgtcacaaac 800  
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 catccctggg gcctcagaca tagatctcat cccacggaa ggggtgaagg 900  
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 agtggagctc tggtcacagt tagcaggaat cccctggaag aaacctcagc 1150  
 cctctctgtt gagacacaa gttacgtcaa agtctcagga gcagctccgg 1200  
 tctccataga ggctgggtca gcagtgggca aaacaacttc ctttgctggg 1250  
 agctctgctt cctcctacag cccctcgga ggcgcctca agaacttcac 1300  
 cccttcagag acaccgacca tggacatgc aaccaagggg cccttccca 1350  
 ccagcagga cctcttctt tctgtcctc cgactacaac caacagcagc 1400  
 cgagggacga acagcacctt agccaagatc acaacctcag cgaagaccac 1450  
 gatgaagccc caacagccac gccacgact gcccgacga ggccgaccac 1500  
 agacgtgagt gcaggtgaaa atggaggttt cctcctcctg cggtgagtg 1550  
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 cagcagctcc accgggaact ccacgccac gcgcctcact tccaggtctc 1650  
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 gactgcagct gcgttactgt gctgagaggt acccagaagg tttccatgaa 1800  
 gggcagcatg tccaagcccc taacccaga tgtggcaaca ggaccctgc 1850  
 tcacatccac cggagtgtat gtatggggag gggcttcacc tgttcccaga 1900

gggtgtccttg gactcacctt ggcacatggt ctgtgtttca gtaaagagag 1950  
acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttcactcagt 2000  
gtggcccaaa aaaaa 2015

<210> 513  
<211> 482  
<212> PRT  
<213> Homo Sapien

<400> 513  
Met Gly Cys Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys  
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20 25 30  
Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala  
35 40 45  
Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu  
50 55 60  
Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile  
65 70 75  
Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg  
80 85 90  
Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu  
95 100 105  
Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu  
110 115 120  
Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro  
125 130 135  
Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu  
140 145 150  
Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr  
155 160 165  
Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser  
170 175 180  
Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser  
185 190 195  
Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg  
200 205 210  
Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile  
215 220 225  
Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu  
230 235 240  
Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile  
245 250 255

Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	Asp	260	265	270
Ile	Asp	Leu	Ile	Pro	Thr	Glu	Gly	Val	Lys	Ala	Ser	Ser	Thr	Ser	275	280	285
Asp	Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	290	295	300
Thr	Glu	Val	Thr	Ala	Ser	Ala	Glu	Thr	Leu	Ser	Thr	Ala	Gly	Thr	305	310	315
Thr	Glu	Ser	Ala	Ala	Pro	His	Ala	Thr	Val	Gly	Thr	Pro	Leu	Pro	320	325	330
Thr	Asn	Ser	Ala	Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr	335	340	345
Thr	Leu	Ser	Gly	Ala	Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu	350	355	360
Glu	Thr	Ser	Ala	Leu	Ser	Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val	365	370	375
Ser	Gly	Ala	Ala	Pro	Val	Ser	Ile	Glu	Ala	Gly	Ser	Ala	Val	Gly	380	385	390
Lys	Thr	Thr	Ser	Phe	Ala	Gly	Ser	Ser	Ala	Ser	Ser	Tyr	Ser	Pro	395	400	405
Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr	Pro	Ser	Glu	Thr	Pro	Thr	410	415	420
Met	Asp	Ile	Ala	Thr	Lys	Gly	Pro	Phe	Pro	Thr	Ser	Arg	Asp	Pro	425	430	435
Leu	Pro	Ser	Val	Pro	Pro	Thr	Thr	Thr	Asn	Ser	Ser	Arg	Gly	Thr	440	445	450
Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys	Thr	Thr	Met	455	460	465
Lys	Pro	Gln	Gln	Pro	Arg	Pro	Arg	Leu	Pro	Gly	Arg	Gly	Arg	Pro	470	475	480

Gln Thr

<210> 514  
 <211> 2284  
 <212> DNA  
 <213> Homo Sapien

<400> 514  
 gcggagcatc cgetgcggtc ctgcgcgaga ccccgcgcg gattcgccgg 50  
 tccttcccg cggcgcgaca gagctgtcct cgcaoctgga tggcagcagg 100  
 ggcgcgggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150  
 cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200  
 gaccaaaact aaactgaaat ttaaaatggt ctctggggga gaaggagct 250

tgacttacac tttggaata atttgcttcc tgacactaag gctgtctgct 300  
 agtcagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350  
 gtcattctctt tctaagggaa tcagaggcaa tgagcccgtata tacaattcaa 400  
 ctcaagaaga ctgcattaat tcttgctgtt caacaaaaaa catatcaggg 450  
 gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500  
 acccaactgc tacctatattt tctgtcccaa cgaggaagcc tgtccattga 550  
 aaccagcaaa aggacttatg agttacagga taattacaga ttttccatct 600  
 ttgaccagaa atttgccaag ccaagagtta cccaggaag attctctctt 650  
 acatggccaa ttttcacaag cagtcactcc cctagcccat catcacacag 700  
 attattcaaa gccacccgat atctcatgga gagacacact ttctcagaag 750  
 tttggatcct cagatcacct ggagaaacta ttttaagatgg atgaagcaag 800  
 tgcccagctc cttgcttata aggaaaaagg ccattctcag agttcacaat 850  
 tttcctctga tcaagaaata gctcatctgc tgcctgaaaa tgtgagtgcg 900  
 ctcccagcta cgggtggcagt tgcttctcca cataccacct cggctactcc 950  
 aaagcccgcc acccttctac ccaccaatgc ttcagtgaca ctttctggga 1000  
 cttcccagcc acagctggcc accacagctc cacctgtaac cactgtcact 1050  
 tctcagcctc ccacgacct catttctaca gtttttacac gggctgcggc 1100  
 tacaactcaa gcaatggcta caacagcagt tctgactacc acctttcagg 1150  
 cacctacgga ctcgaaaggc agcttagaaa ccataccgtt tacagaaatc 1200  
 tccaacttaa ctttgaacac agggaatgtg tataacccta ctgcactttc 1250  
 tatgtcaaat gtggagtctt ccactatgaa taaaactgct tcctgggaag 1300  
 gtagggaggc cagtccaggc agttcctccc agggcagtggt tccagaaaat 1350  
 cagtacggcc ttccatttga aaaatggctt cttatcgggt ccctgctctt 1400  
 tgggtgtctg ttctgtgtga taggcctcgt cctcctgggt agaatccttt 1450  
 cggaatcact ccgcaggaaa cgttactcaa gactggatta tttgatcaat 1500  
 gggatctatg tggacatcta aggatggaac tcggtgtctc ttaattcatt 1550  
 tagtaaccag aagcccaaat gcaatgagtt tctgctgact tgctagtctt 1600  
 agcaggaggt tgtattttga agacaggaaa atgccccctt ctgctttcct 1650  
 tttttttttt ggagacagag tcttgctctg ttgcccaggc tggagtgcag 1700  
 tagcacgata tcggctctca ccgcaacctc cgtctcctgg gttaagcga 1750  
 ttctcctgcc tcagcctcct aagtatctgg gattacaggc atgtgccacc 1800  
 acacctgggt gatttttgta ttttagtag agacgggggt tcaccatggt 1850

gggtcaggctg gtctcaaact cctgacctag tgatccaccc tcctcggcct 1900  
 cccaaagtgc tgggattaca ggcattgagcc accacagctg gcccccttct 1950  
 gttttatgtt tggtttttga gaaggaatga agtgggaacc aaattaggta 2000  
 attttgggta atctgtctct aaaatattag ctaaaaacaa agctctatgt 2050  
 aaagtaataa agtataattg ccatataaat ttcaaaattc aactggcttt 2100  
 tatgcaaaga aacagggttag gacatctagg ttccaattca ttcacattct 2150  
 tggttccaga taaaatcaac tggtttatct aatttctaata ggatttgctt 2200  
 ttctttttat atggattcct ttaaaactta ttccagatgt agttccttcc 2250  
 aattaaatat ttgaataaat cttttgttac tcaa 2284

<210> 515  
 <211> 431  
 <212> PRT  
 <213> Homo Sapien

<400> 515  
 Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile  
 1 5 10 15  
 Ile Cys Phe Leu Thr Leu Arg Leu Ser Ala Ser Gln Asn Cys Leu  
 20 25 30  
 Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu  
 35 40 45  
 Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln  
 50 55 60  
 Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly  
 65 70 75  
 Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala  
 80 85 90  
 Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala  
 95 100 105  
 Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile  
 110 115 120  
 Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu  
 125 130 135  
 Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val  
 140 145 150  
 Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp  
 155 160 165  
 Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp  
 170 175 180  
 His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu  
 185 190 195

Leu	Ala	Tyr	Lys	Glu	Lys	Gly	His	Ser	Gln	Ser	Ser	Gln	Phe	Ser	
				200					205					210	
Ser	Asp	Gln	Glu	Ile	Ala	His	Leu	Leu	Pro	Glu	Asn	Val	Ser	Ala	
				215					220					225	
Leu	Pro	Ala	Thr	Val	Ala	Val	Ala	Ser	Pro	His	Thr	Thr	Ser	Ala	
				230					235					240	
Thr	Pro	Lys	Pro	Ala	Thr	Leu	Leu	Pro	Thr	Asn	Ala	Ser	Val	Thr	
				245					250					255	
Pro	Ser	Gly	Thr	Ser	Gln	Pro	Gln	Leu	Ala	Thr	Thr	Ala	Pro	Pro	
				260					265					270	
Val	Thr	Thr	Val	Thr	Ser	Gln	Pro	Pro	Thr	Thr	Leu	Ile	Ser	Thr	
				275					280					285	
Val	Phe	Thr	Arg	Ala	Ala	Ala	Thr	Leu	Gln	Ala	Met	Ala	Thr	Thr	
				290					295					300	
Ala	Val	Leu	Thr	Thr	Thr	Phe	Gln	Ala	Pro	Thr	Asp	Ser	Lys	Gly	
				305					310					315	
Ser	Leu	Glu	Thr	Ile	Pro	Phe	Thr	Glu	Ile	Ser	Asn	Leu	Thr	Leu	
				320					325					330	
Asn	Thr	Gly	Asn	Val	Tyr	Asn	Pro	Thr	Ala	Leu	Ser	Met	Ser	Asn	
				335					340					345	
Val	Glu	Ser	Ser	Thr	Met	Asn	Lys	Thr	Ala	Ser	Trp	Glu	Gly	Arg	
				350					355					360	
Glu	Ala	Ser	Pro	Gly	Ser	Ser	Ser	Gln	Gly	Ser	Val	Pro	Glu	Asn	
				365					370					375	
Gln	Tyr	Gly	Leu	Pro	Phe	Glu	Lys	Trp	Leu	Leu	Ile	Gly	Ser	Leu	
				380					385					390	
Leu	Phe	Gly	Val	Leu	Phe	Leu	Val	Ile	Gly	Leu	Val	Leu	Leu	Gly	
				395					400					405	
Arg	Ile	Leu	Ser	Glu	Ser	Leu	Arg	Arg	Lys	Arg	Tyr	Ser	Arg	Leu	
				410					415					420	
Asp	Tyr	Leu	Ile	Asn	Gly	Ile	Tyr	Val	Asp	Ile					
				425					430						

<210> 516  
 <211> 2749  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> unsure  
 <222> 1869, 1887  
 <223> unknown base

<400> 516  
 ctcccacggt gtccagcgcc cagaatgcgg cttctggtcc tgctatgggg 50  
 ttgctgctg ctcccaggtt atgaagccct ggagggccca gaggaatatca 100

gggggttcga aggggacact gtgtccctgc agtgcacctc cagggaagag 150  
 ctgagggacc accggaagta ctggtgcagg aaggggtggga tcctcttctc 200  
 tcgtgtctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250  
 agggcaggggt gtccatccgt gacagccgcc aggagctctc gtcattgtg 300  
 accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggt 350  
 cgaaaaacgg ggccccgatg agtctttact gatctctctg ttctgttttc 400  
 caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctggct 450  
 acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agcccccagg 500  
 attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550  
 agacaggggc tgaggcccct ccattgccag ggacttccca gtacgggcac 600  
 gaaaggactt ctcagtacac aggaacctct cctcaccag cgacctctcc 650  
 tcctgcaggg agctcccgcc ccccatgca gctggactcc acctcagcag 700  
 aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750  
 atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800  
 gtcagccgca ggctgatcg ccttctgcag ccacctgctc ctgtggagaa 850  
 aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900  
 tcacgcttga ctgcgaggga aaaggaagcc ccttcccagg ccctgaggg 950  
 ggacgtgatc tcgatgcctc ccctccacac atctgaggag gagctgggct 1000  
 tctcgaagtt tgtctcagcg tagggcagga ggccctcctg gccaggccag 1050  
 cagtgaagca gtatggctgg ctggatcagc accgattccc gaaagctttc 1100  
 cacctcagcc tcagagtcca gctgcccgga ctccagggtc ctccccaccc 1150  
 tccccaggct ctctcttgc atgttccagc ctgacctaga agcgtttgtc 1200  
 agccctggag ccagagcgg tggccttget cttccggctg gagactggga 1250  
 catccctgat aggttcacat ccctgggcag agtaccaggc tgctgaccct 1300  
 cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350  
 aggaactcct gggcctcatg cccagtgtcg gacctgcct tcctcccact 1400  
 ccagaoccca ccttgtcttc cctccctggc gtctcagac ttagtcccac 1450  
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 ggattctggc ttctctttga accacctgca tccagccctt caggaagcct 1550  
 gtgaaaaacg tgattcctgg cccaccaag accaccaaa accatctctg 1600  
 ggcttgggtgc aggactctga attotaacaa tgcccagtga ctgtcgcaact 1650  
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 acagaagtgg ttgcctttnc catttgccct ccttgncca tgccttcttg 1900  
 cctttggaaa aaatgatgaa gaaaacctg gctccttcct tgtctggaaa 1950  
 gggttacttg cctatgggtt ctggtggcta gagagaaaag tagaaaacca 2000  
 gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050  
 ctgaaggtga ctccgagtcc agccccctgg agaaggggtc gggggtggtg 2100  
 gtaaagtagc acaactacta ttttttttct ttttccatta ttattgtttt 2150  
 ttaagacaga atctcgtgct gctgcccagg ctggagtga gtggcacgat 2200  
 ctgcaaactc cgctcctgg gttcaagtga ttcttctgcc tcagcctccc 2250  
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 cttttagtag agatgggggtt tcaccatggt ggccaggctg gtcttgaact 2350  
 cctgacctca aatgagcctc ctgcttcagt ctcccaaatt gccgggatta 2400  
 caggcatgag ccaactgtgtc tggccctatt tcctttaaaa agtgaaatta 2450  
 agagttgttc agtatgcaaa acttggaaag atggaggaga aaaagaaaag 2500  
 gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550  
 tttgttgtag ttcttccac tcttttcttc ttacataat ttgccggtgt 2600  
 tctttttaca gagcaattat cttgtatata caactttgta tctgccttt 2650  
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 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 517  
 <211> 332  
 <212> PRT  
 <213> Homo Sapien

<400> 517  
 Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly  
 1 5 10 15  
 Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly  
 20 25 30  
 Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp  
 35 40 45  
 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg  
 50 55 60  
 Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met  
 65 70 75

Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu	80	85	90
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr	95	100	105
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	110	115	120
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	125	130	135
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	140	145	150
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	155	160	165
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	170	175	180
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	185	190	195
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro	200	205	210
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala	215	220	225
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg	230	235	240
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu	245	250	255
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His	260	265	270
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln	275	280	285
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys	290	295	300
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro	305	310	315
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val	320	325	330

Ser Ala

<210> 518

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

ccctgcagtg cacctacagg gaag 24

<210> 519

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

ctgtcttccc ctgcttggt gtgg 24

<210> 520

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ggtgcaggaa ggggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 521

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

ccagtgcaca gcaggcaacg aagc 24

<210> 522

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 522

actaggctgt atgcctgggt gggc 24

<210> 523

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 523

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 524

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe  
<400> 524  
aatctcagca ccagccactc agagca 26  
<210> 525  
<211> 25  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
<400> 525  
gttaaagagg gtgcccttcc agcga 25  
<210> 526  
<211> 24  
<212> DNA  
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